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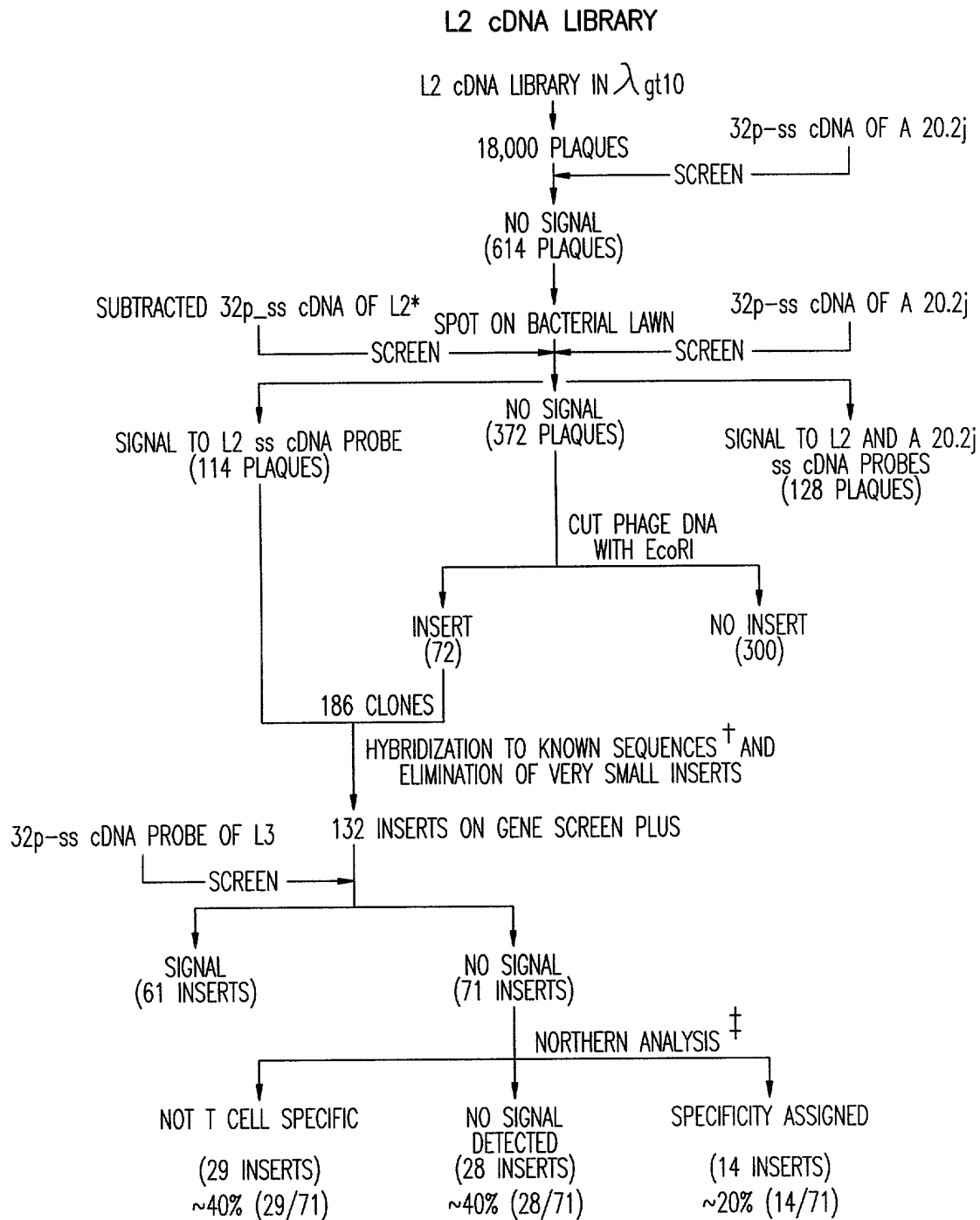


FIG. 1A

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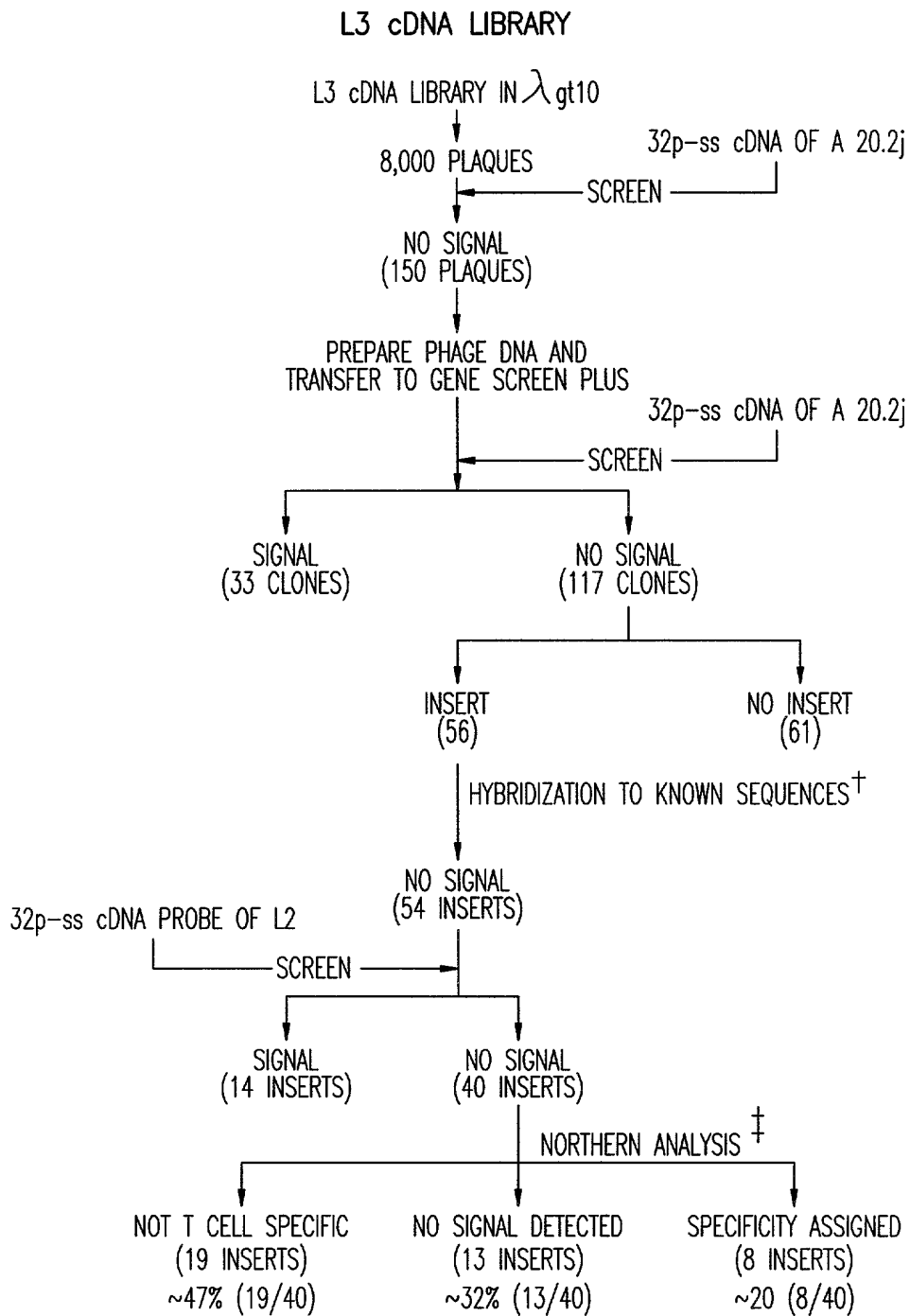


FIG. 1B

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-145 ATGTC

-140 CATGAACTGC TGAGTGCATA AACAGCACGG GATATCTCTG TCTAAAGGAA TATTACTACA CCAGGAAAAG

-70 GACACATTCG ACAACAGGAA AGGAGCCTGT CACAGAAAAC CACAGTGTCC TGTGCATGTG ACATTTCGCC

1 ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG GGC TGT GAG AAG 60  
1 Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val Gly Cys Glu Lys 20

61 GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC TGT CAG CCT GGT ACT TTC TGC AGA AAA TAC 120  
21 Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys Tyr 40

121 AAT CCA GTC TGC AAG AGC TGC CCT CCA AGT ACC TTC TCC AGC ATA GGT GGA CAG CCG AAC 180  
41 Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn 60

181 TGT AAC ATC TGC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT ACC 240  
61 Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr 80

241 CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA 300  
81 His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg 100

301 TGT GAA AAG GAC TGC AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT AGC 360  
101 Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser 120

361 TTG GGA ACA TTT AAT GAC CAG AAC GGT ACT GGC GTC TGT CGA CCC TGG ACG AAC TGC TCT 420  
121 Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser 140

421 CTA GAC GGA AGG TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC 480  
141 Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro 160

481 CCT GTG GTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GGA 540  
161 Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly 180

541 GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG CTG ACA TCG GCT TTG CTG CTG GCC 600  
181 Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser Ala Leu Leu Leu Ala 200

601 CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC 660  
201 Leu Ile Phe Ile Thr Leu Leu Phe Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His 220

661 ATA TTC AAG CAA CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC 720  
221 Ile Phe Lys Gln Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser 240

721 TGC CGA TGT CCA CAG GAA GAA GAA GGA GGA GGA GGC TAT GAG CTG TGA TGTACTATC 780  
241 Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu ---

FIG. 2A

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781 CTAGGAGATG TGTGGGCCGA AACCGAGAAG CACTAGGACC CCACCATCCT GTGGAACAGC ACAAGCAACC 850  
851 CCACCACCCT GTTCTTACAC ATCATCCTAG ATGATGTGTG GCGCGGCACC TCATCCAAGT CTCTTCTAAC 920  
921 GCTAACATAT TTGTCTTTAC CTTTTTTAAA TCTTTTTTTA AATTTAAATT TTATGTGTGT GAGTGTTTTG 990  
991 CCTGCCTGTA TGCACACGTG TGTGTGTGTG TGTGTGTGAC ACTCCTGATG CCTGAGGAGG TCAGAAGAGA 1060  
1061 AAGGTTGGT TCCATAAGAA CTGGAGTTAT GGATGGCTGT GAGCCGGnnn GATAGGTCGG GACGGAGACC 1130  
1131 TGTCTTCTTA TTTTAACGTG ACTGTATGAT AAAA AAAAAA TGATATTTTCG GGAATTGTAG AGATTGTCCT 1200  
1201 GACACCCTTC TAGTTAATGA TCTAAGAGGA ATTGTTGATA CGTAGTATAC TGTATATGTG TATGTATATG 1270  
1271 TATATGTATA TATAAGACTC TTTTACTGTC AAAGTCAACC TAGAGTGTCT GGTACCAGG TCAATTTTAT 1340  
1341 TGGACATTTT ACGTCACACA CACACACACA CACACACACA CACGTTTATA CTACGTACTGT TATCGGTAT 1410  
1411 TCTACGTCAT ATAATGGGAT AGGGTAAAAG GAAACCAAAG AGTGAGTGAT ATTATTGTGGA GGTGACAGA 1480  
1481 CTACCCCTTC TGGGTACGTA GGGACAGACC TCCTTCGGAC TGTCTAAAAC TCCCCTTAGA AGTCTCGTCA 1550  
1551 AGTCCCGGA CGAAGAGGAC AGAGGAGACA CAGTCCGAAA AGTTATTTT CCGGCAAATC CTTTCCCTGT 1620  
1621 TTCGTGACAC TCCACCCCTT GTGGACACTT GAGTGTGATC CTTGCGCCCG AAGGTCAGGT GGTACCCGTC 1690  
1691 TGTAGGGGCG GGGAGACAGA GCCCGGGGG AGCTACGAGA ATCGACTCAC AGGGCGCCCC GGGCTTCGCA 1760  
1761 AATGAAACTT TTTAATCTC ACAAGTTTCG TCCGGGCTCG GCGGACCTAT GCGCTCGATC CTTATTACCT 1830  
1831 TATCCTGGCG CCAAGATAAA ACAACCAAAA GCCTTGACTC CGGTACTAAT TCTCCCTGCC GGCCCCCGTA 1900  
1901 AGCATAACGC GCGATCTCC ACTTTAAGAA CCTGGCCCGG TTCTGCCTGG TCTCGCTTTC GTAAACGGTT 1970  
1971 CTTACAAAAG TAATTAGTTC TTGCTTTCAG CCTCCAAGCT TCTGCTAGTC TATGGCAGCA TCAAGGCTGG 2040  
2041 TATTTGCTAC GGCTGACCGC TACGCCGCCG CAATAAGGGT ACTGGGCGGC CCGTCGAAGG CCCTTTGGTT 2110  
2111 TCAGAAACCC AAGGCCCCC TCATACCAAC GTTTCGACTT TGATTCTTGC CCGTACGTGG TGGTGGGTGC 2180  
2181 CTTAGCTCTT TCTCGATAGT TAG AC

FIG. 2B

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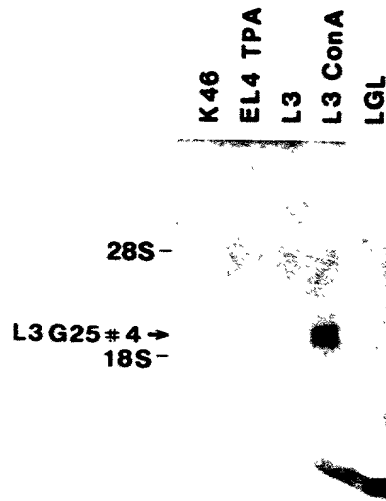


FIG. 3A

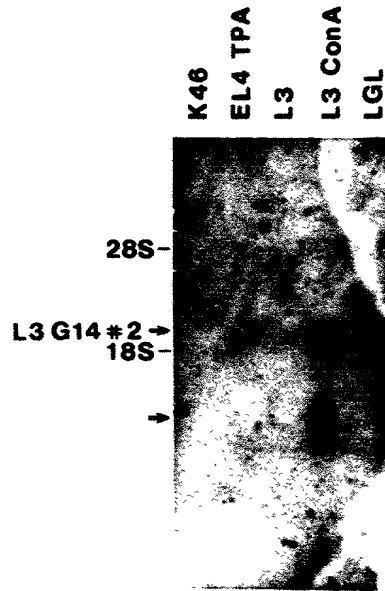


FIG. 3B



FIG. 3C

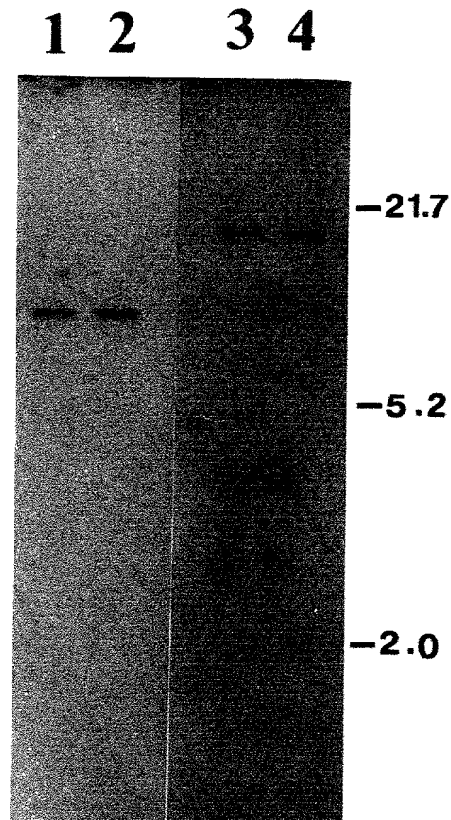


FIG. 4

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K46  
EL4  
EL4 TPA  
L2  
L2 ConA  
L3  
L3 ConA  
LGL

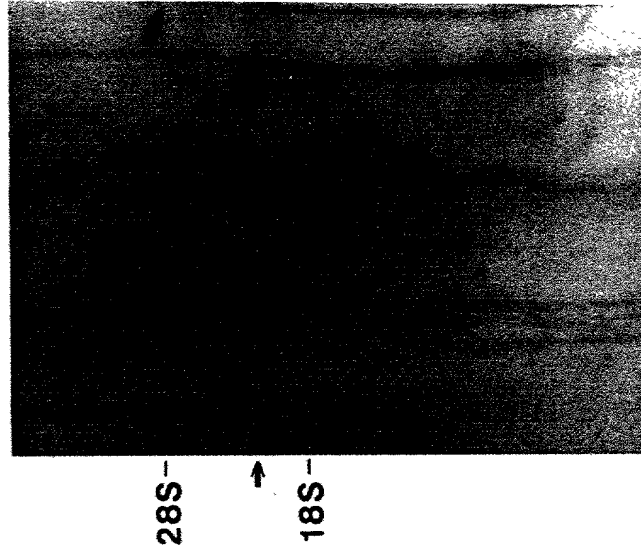


FIG. 5B

K46  
EL4  
EL4 TPA  
L2  
L2 ConA  
L3  
L3 ConA  
LGL

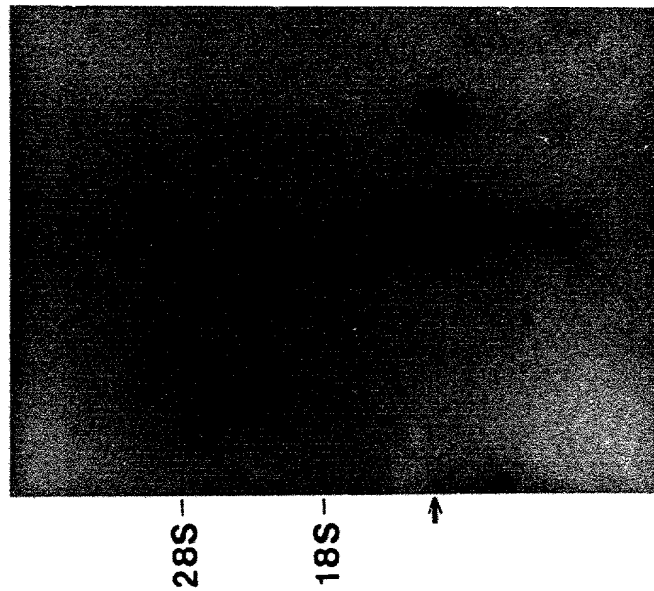


FIG. 5A

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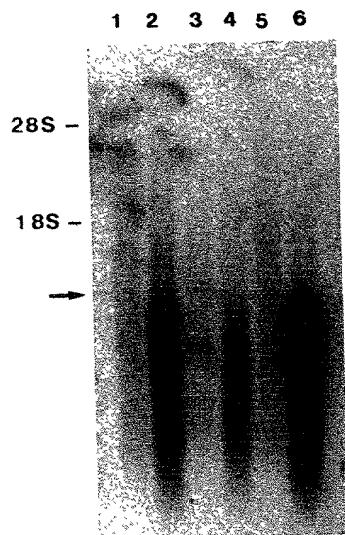


FIG. 7A

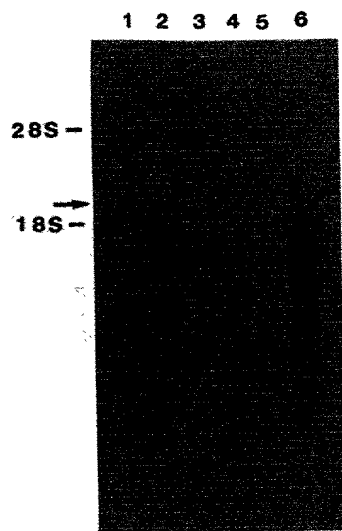


FIG. 7B

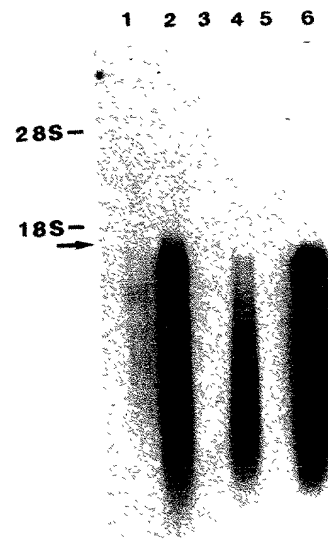


FIG. 7C

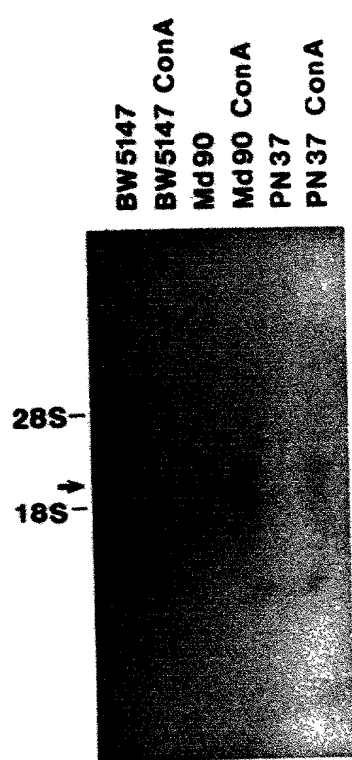


FIG. 8A

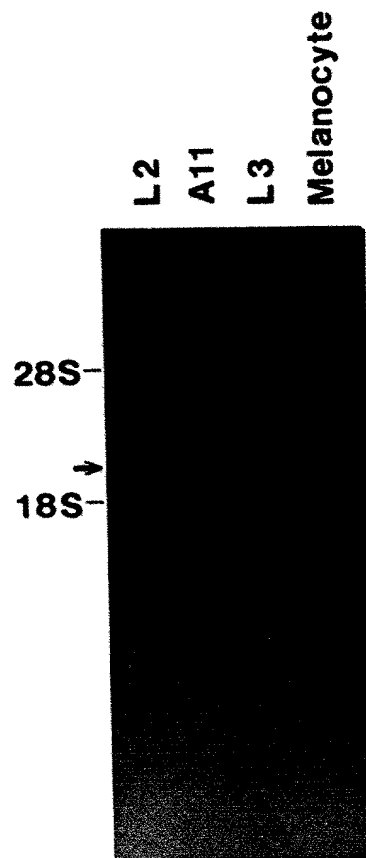
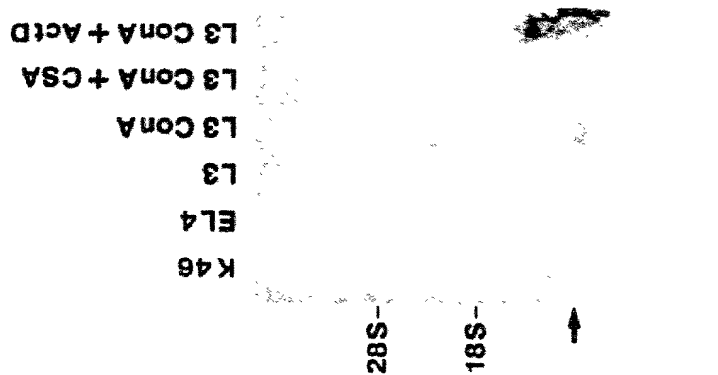
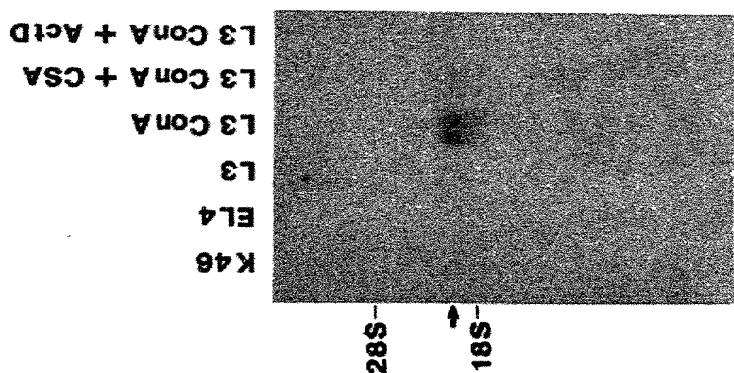
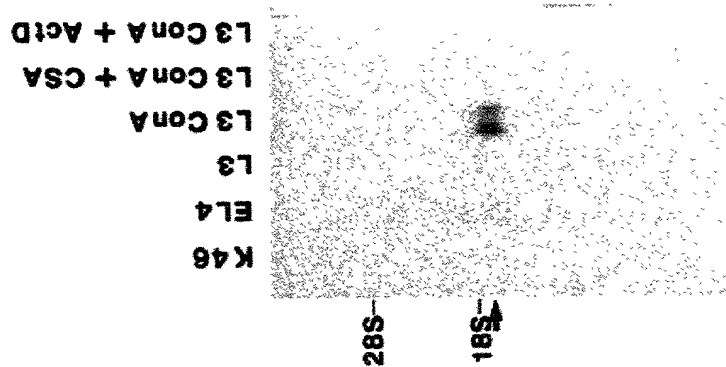
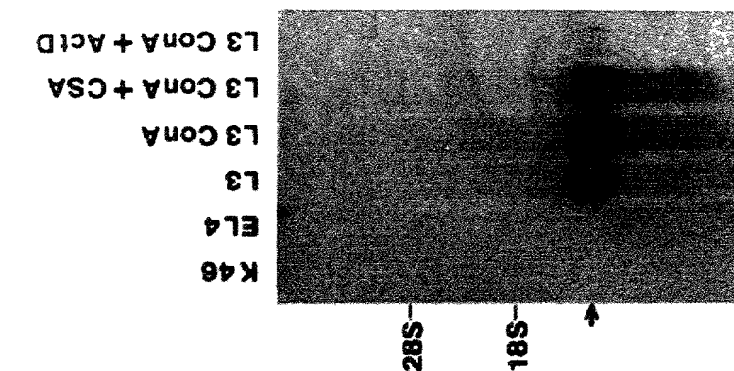


FIG. 8B

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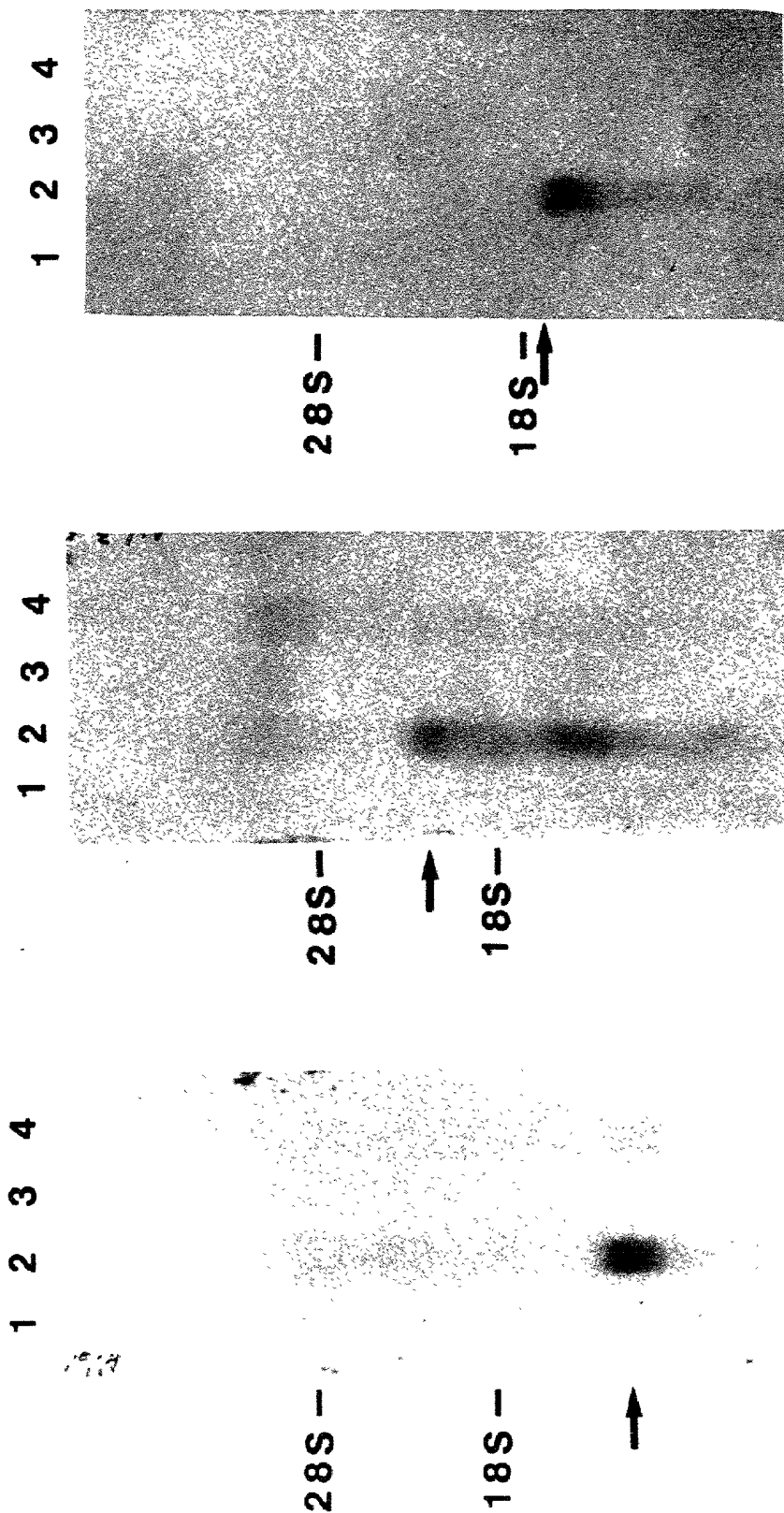


FIG. 10C

FIG. 10B

FIG. 10A

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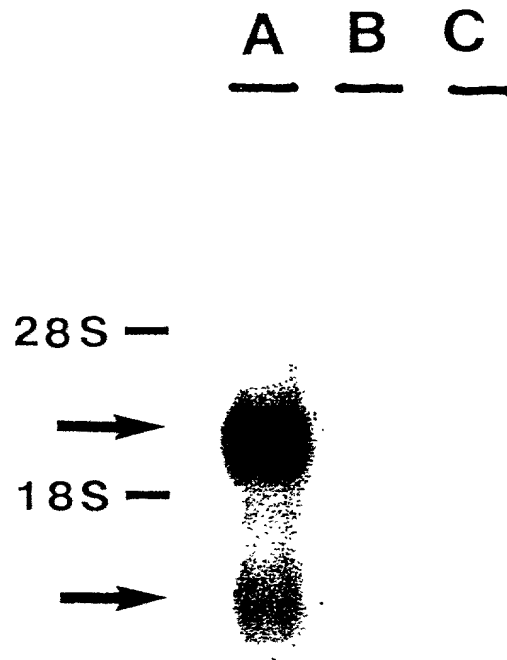


FIG. 11

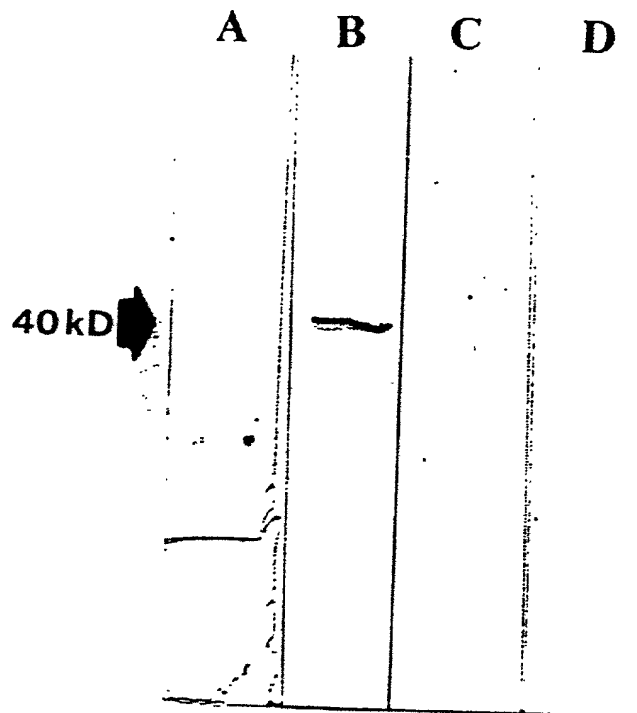


FIG. 12

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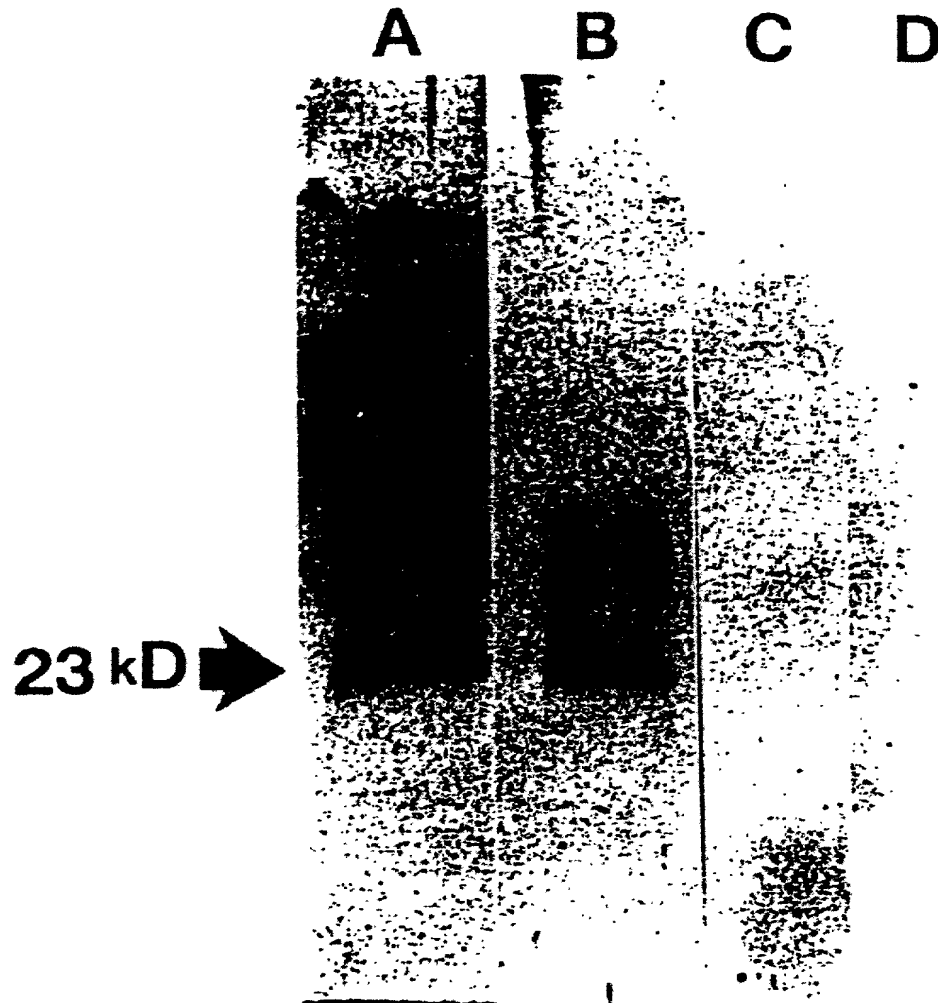


FIG. 13

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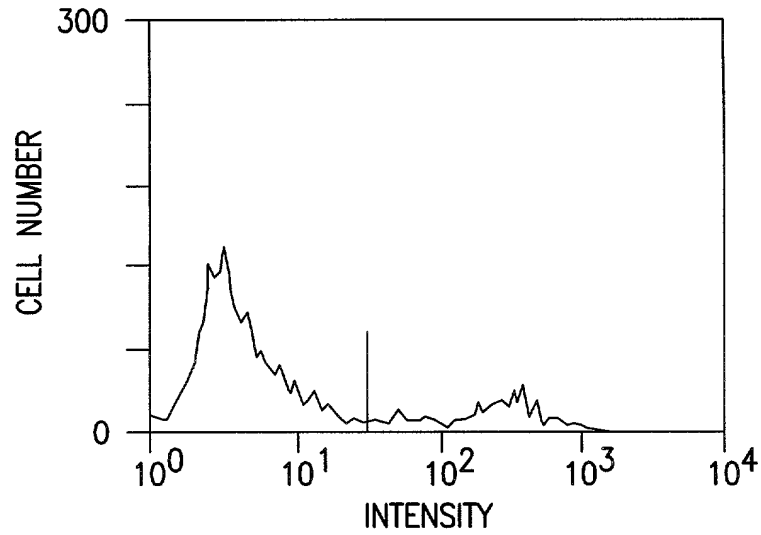


FIG. 14A

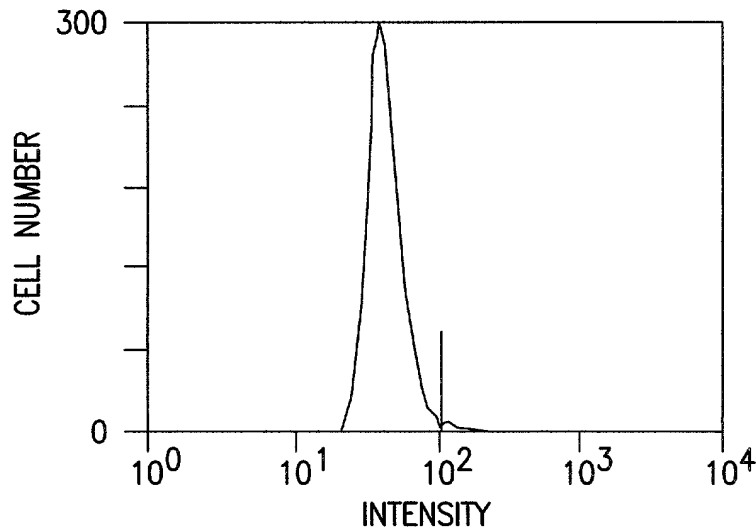


FIG. 14B

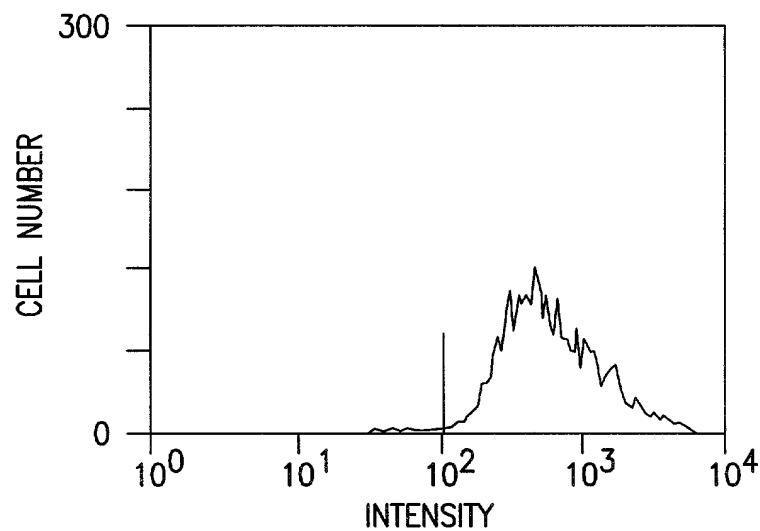


FIG. 14C

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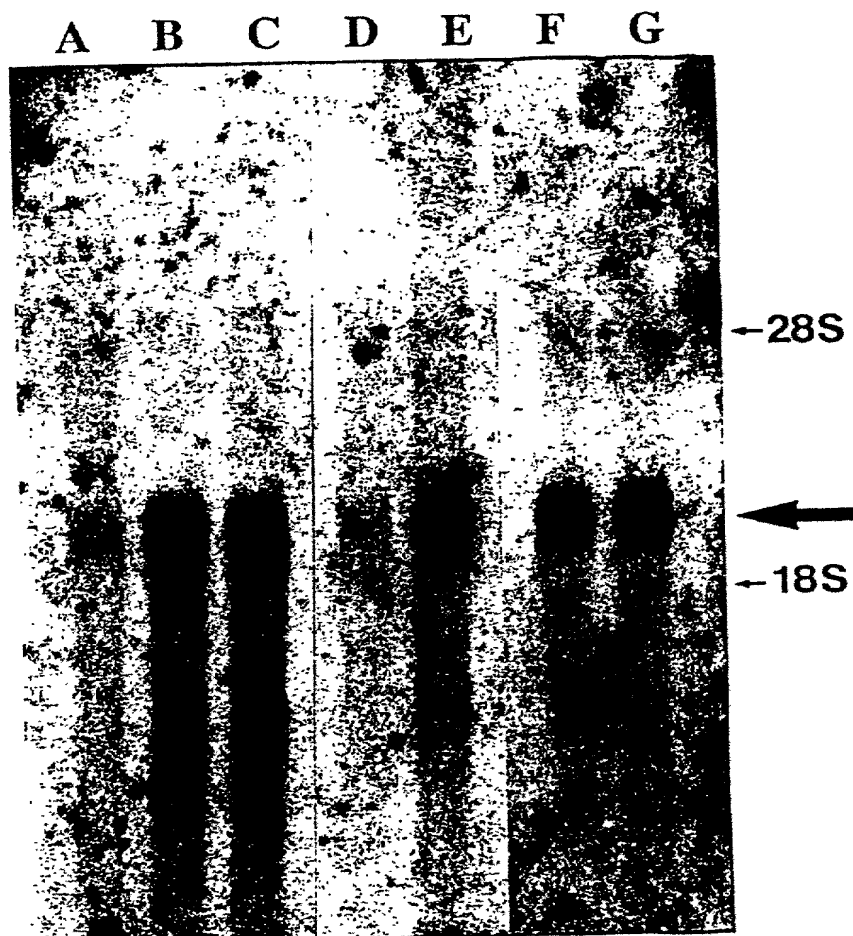


FIG. 15

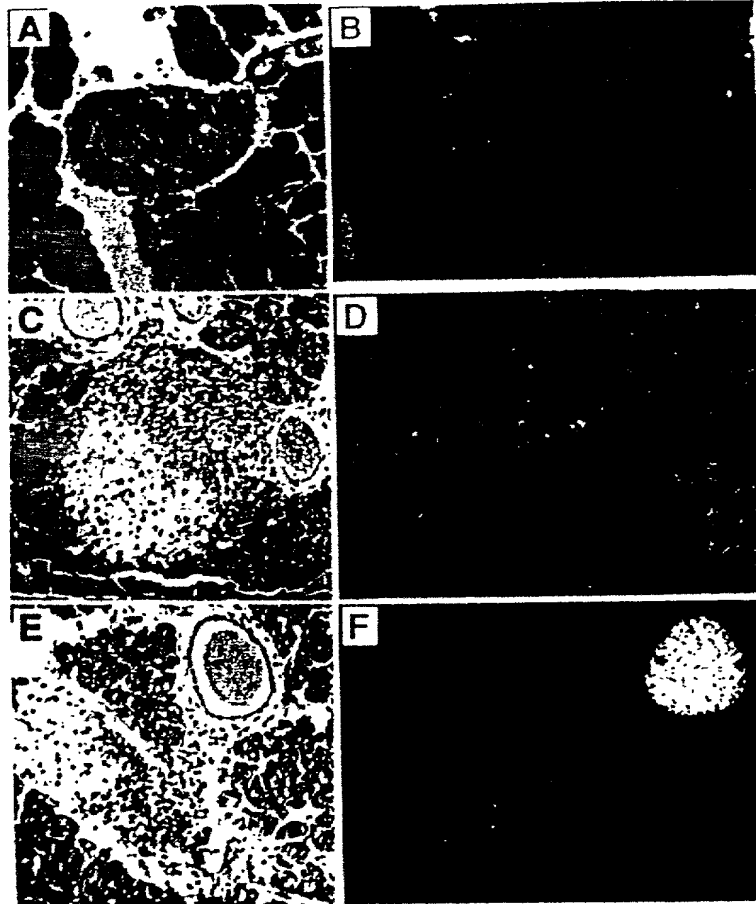


FIG. 16

4-1BB

Sina

DG17

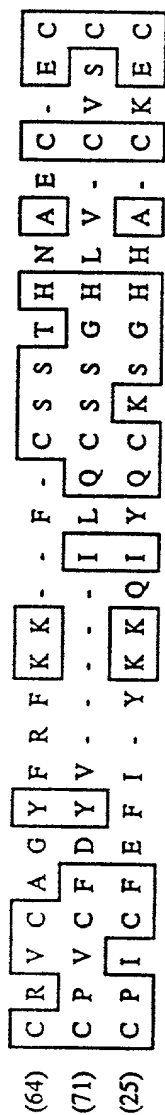


FIG. 17



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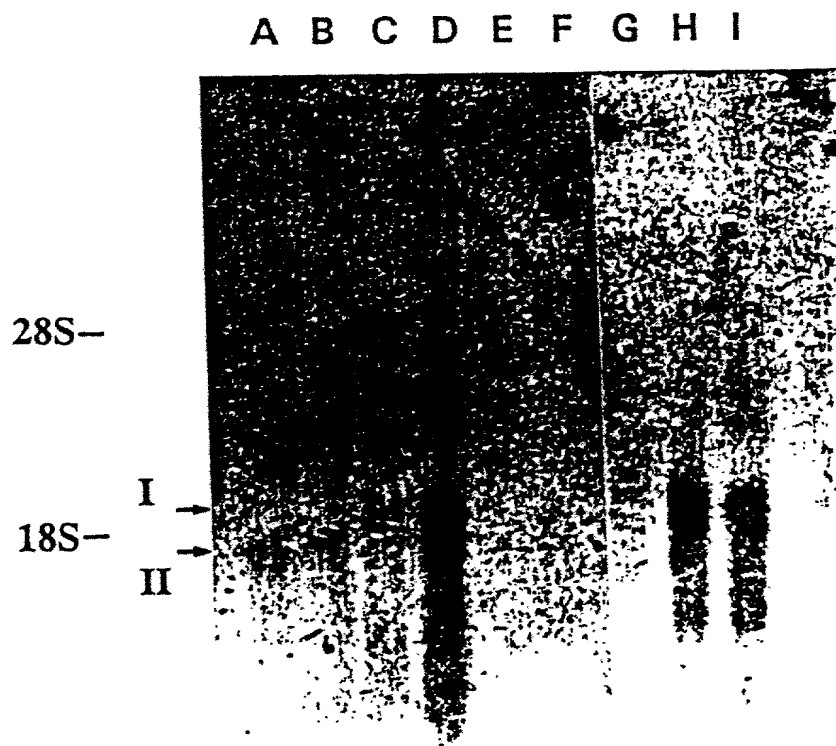


FIG. 18

204020 " 227/9001

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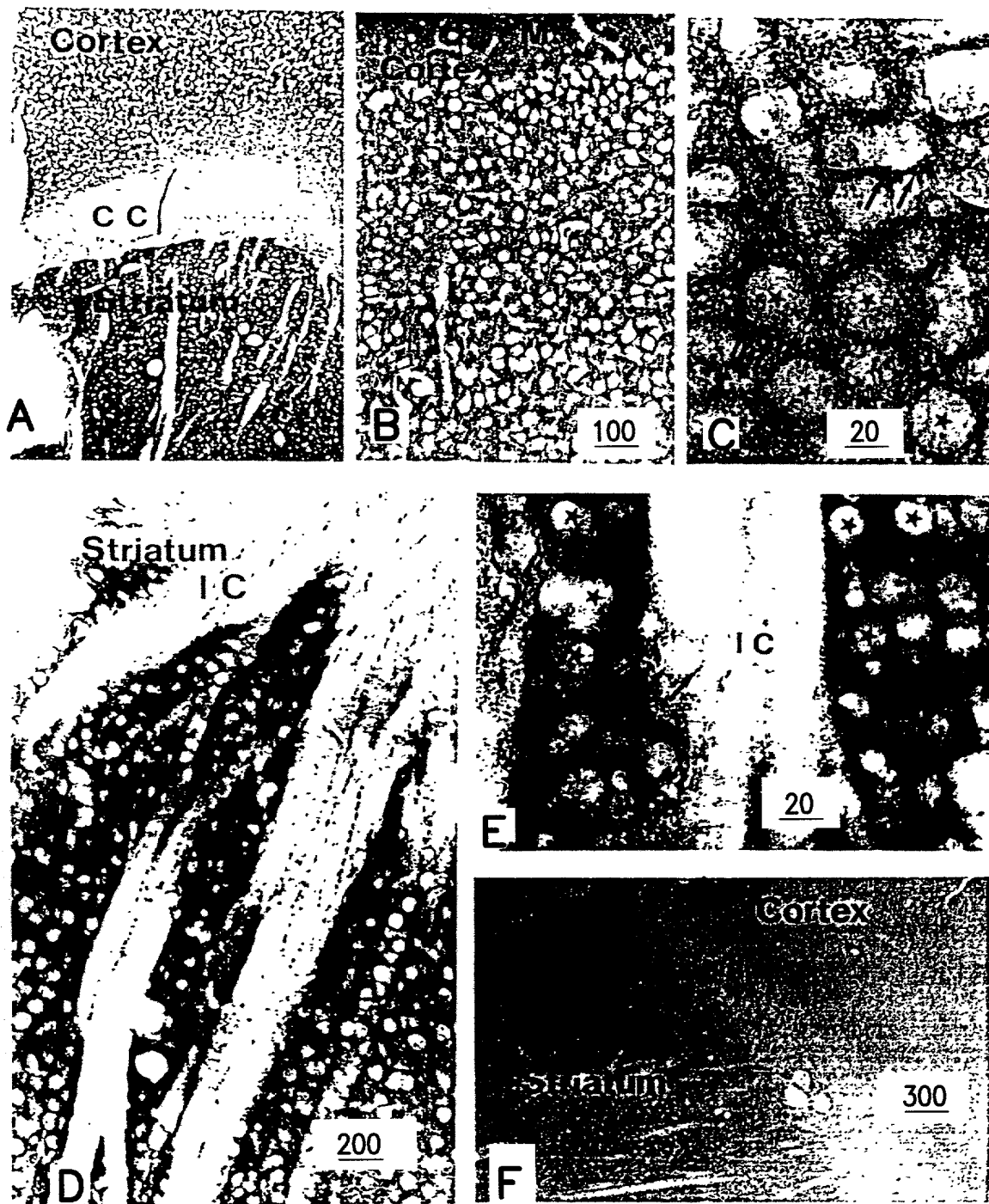


FIG. 19

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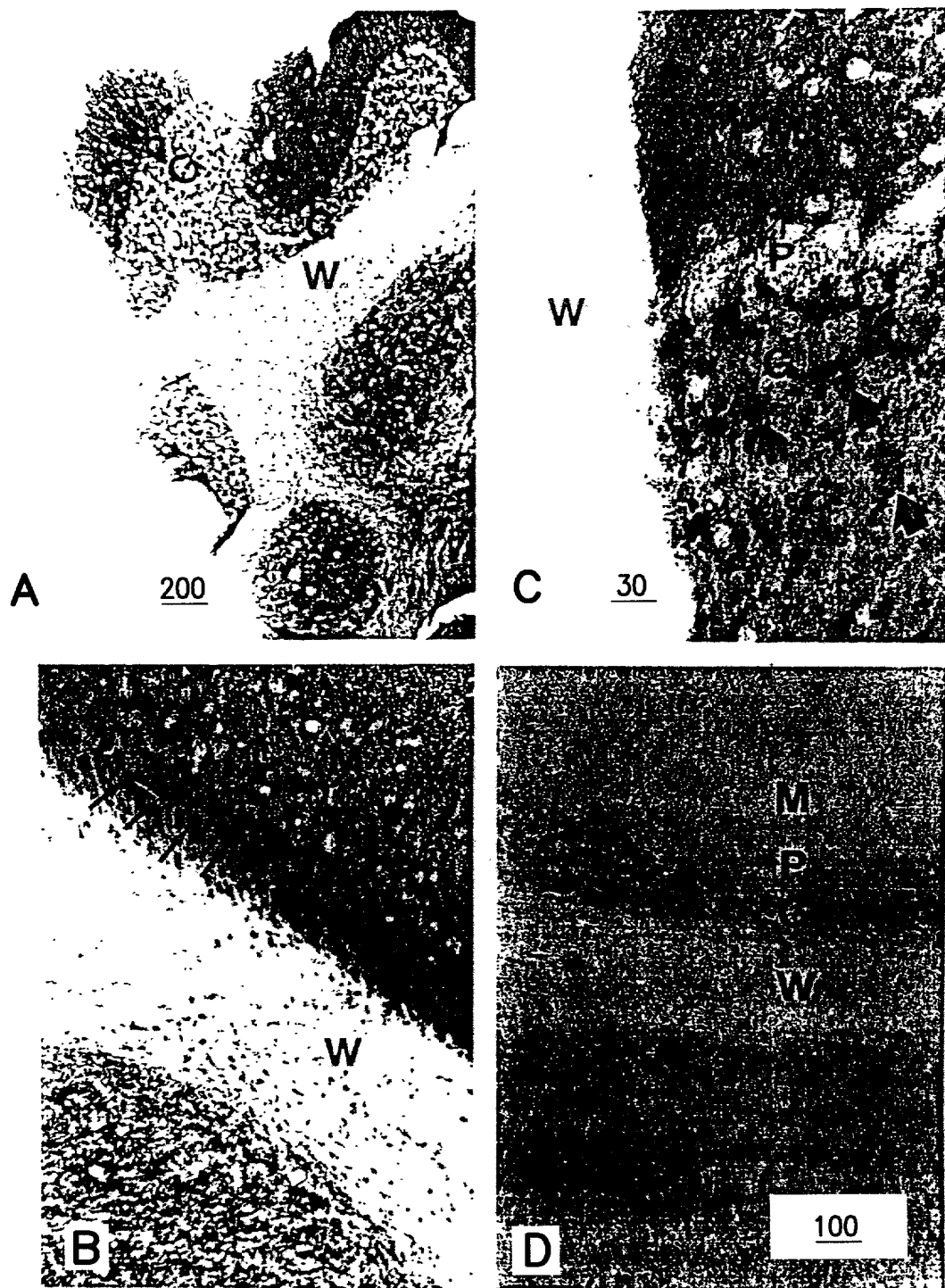


FIG. 20

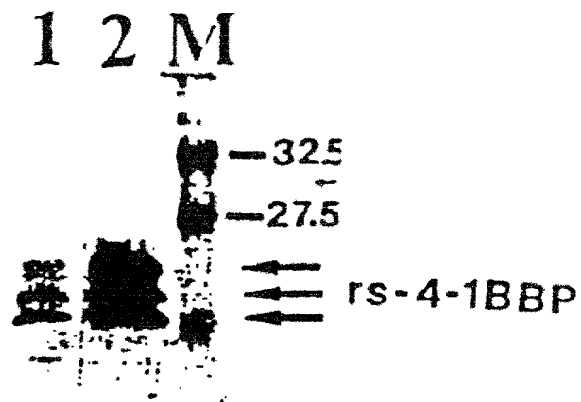


FIG. 21

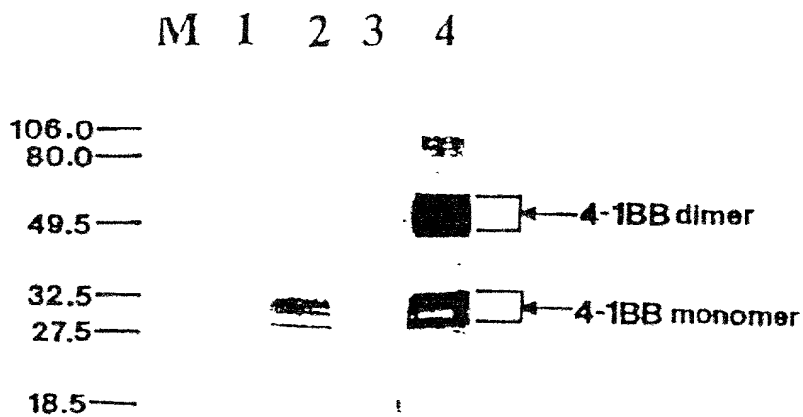


FIG. 22

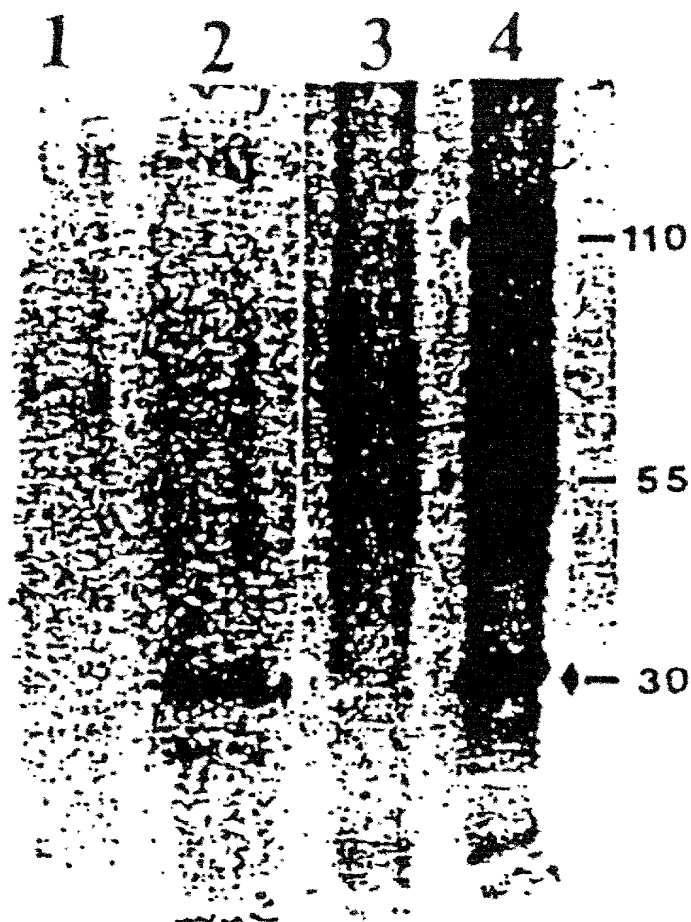


FIG. 23

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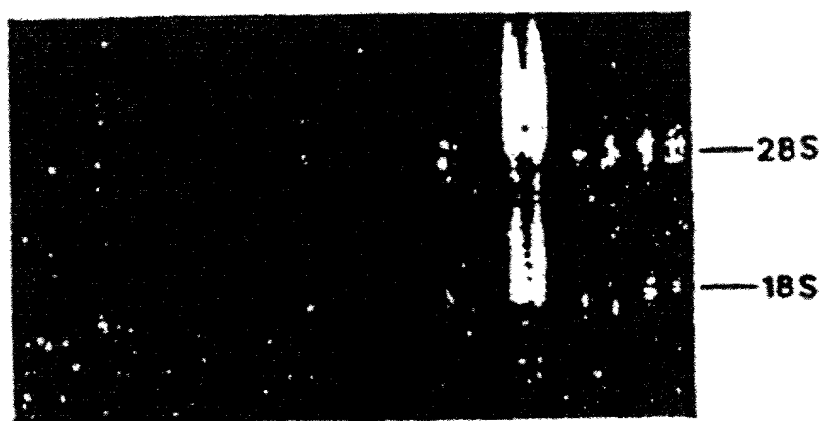


FIG. 25A

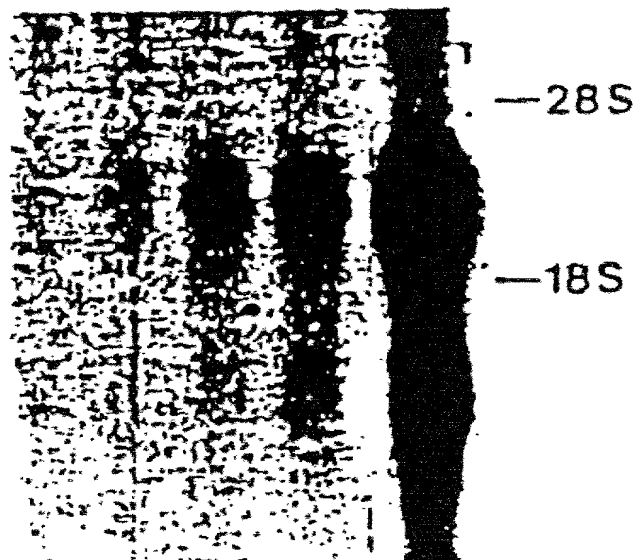
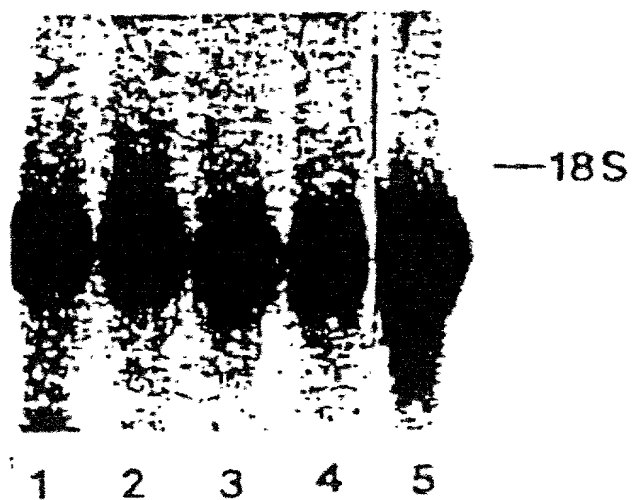


FIG. 25B



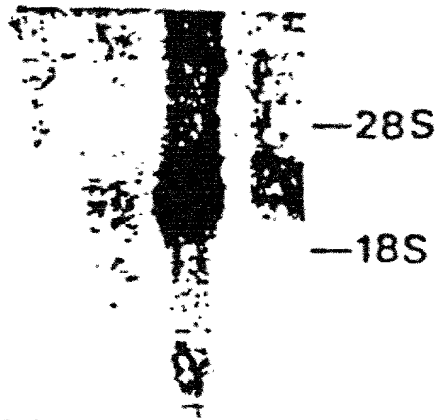


FIG. 26A

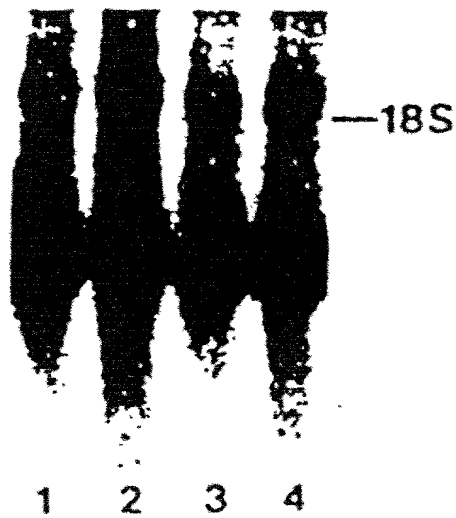


FIG. 26B



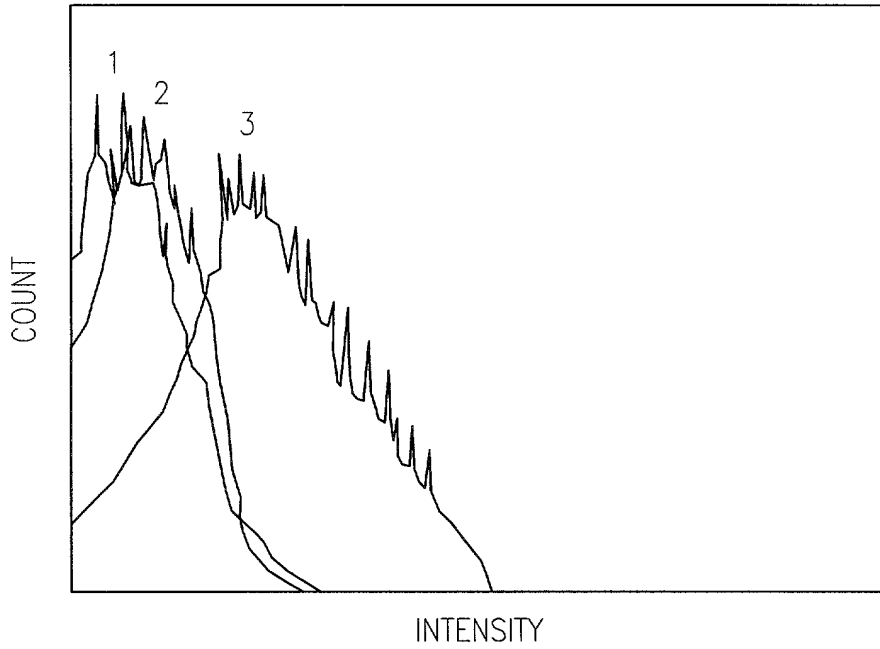


FIG. 27A

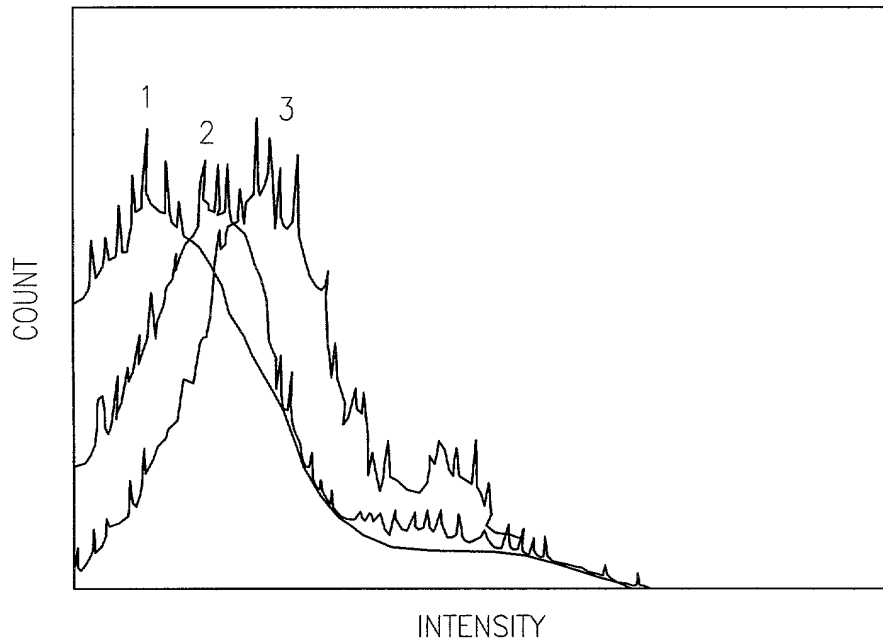


FIG. 27B

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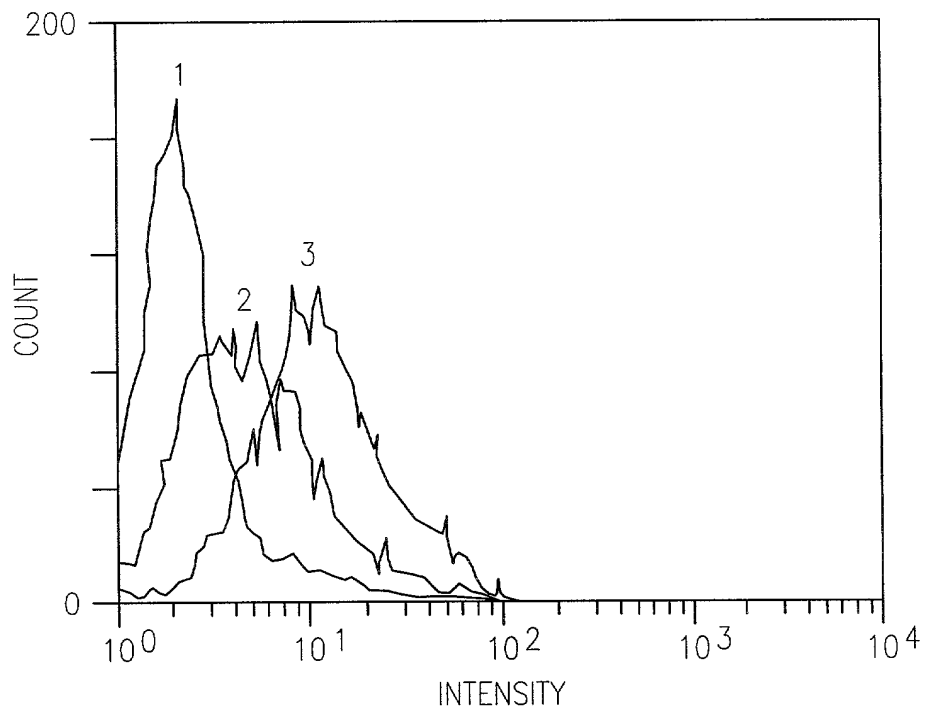


FIG. 27C

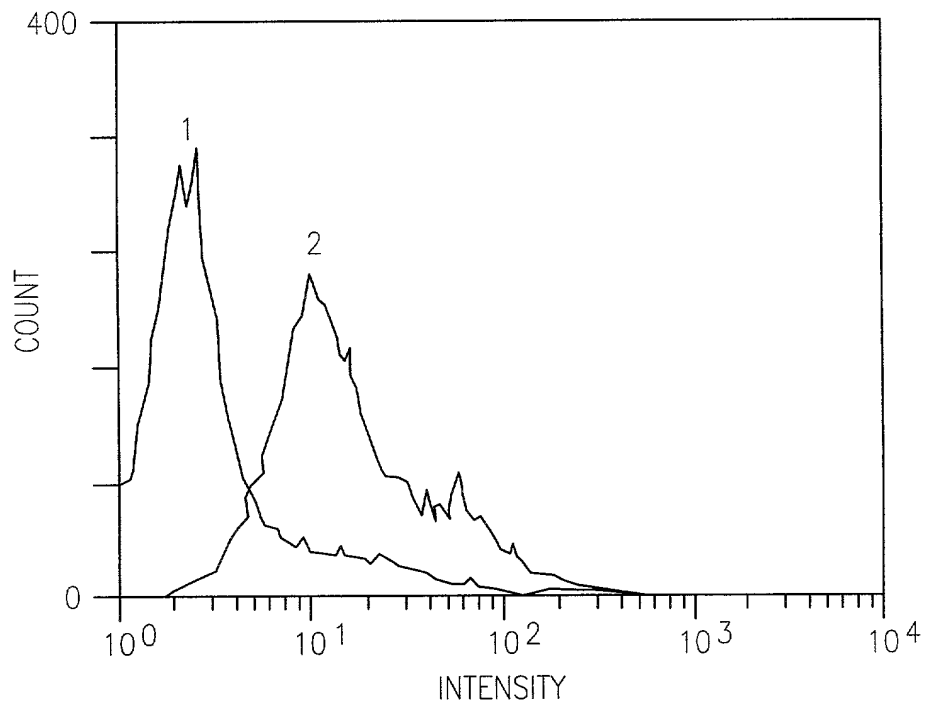


FIG. 27D

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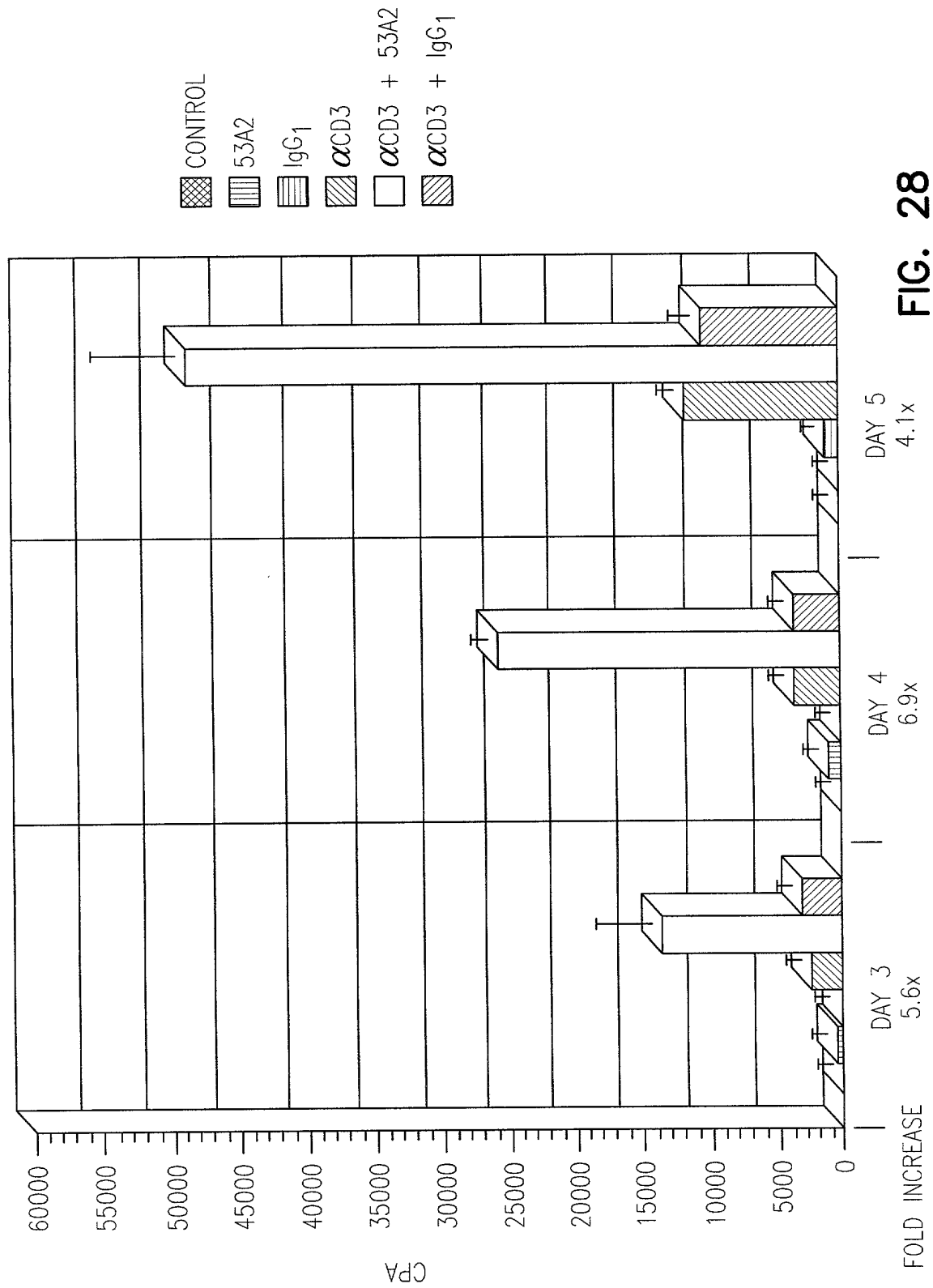


FIG. 28

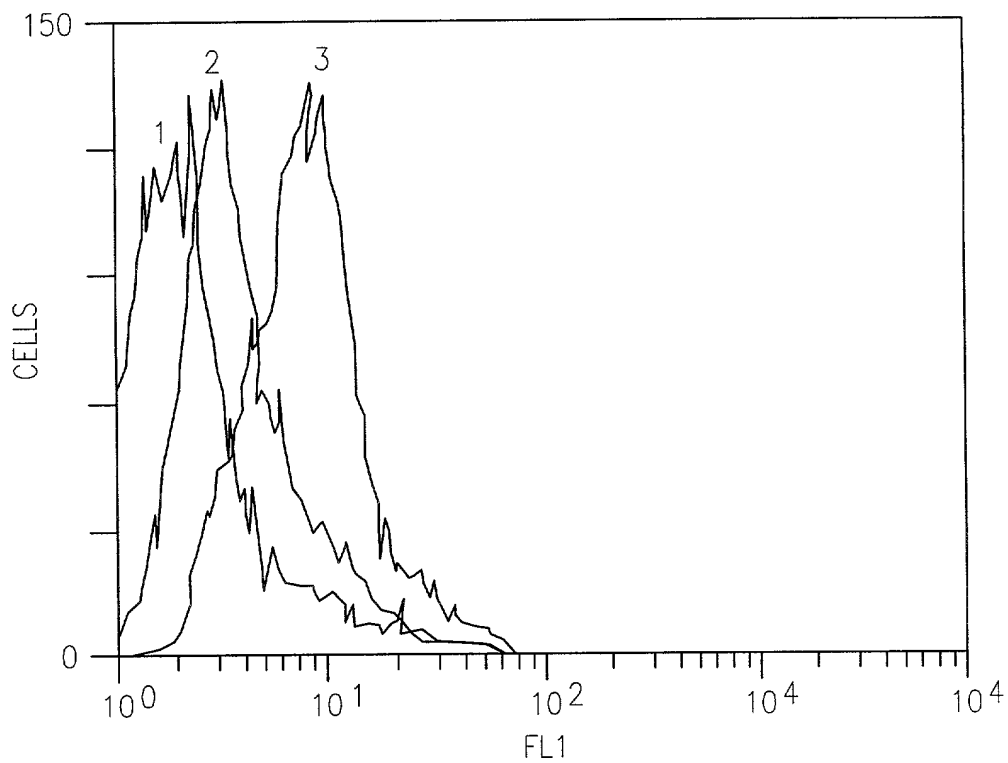


FIG. 29A

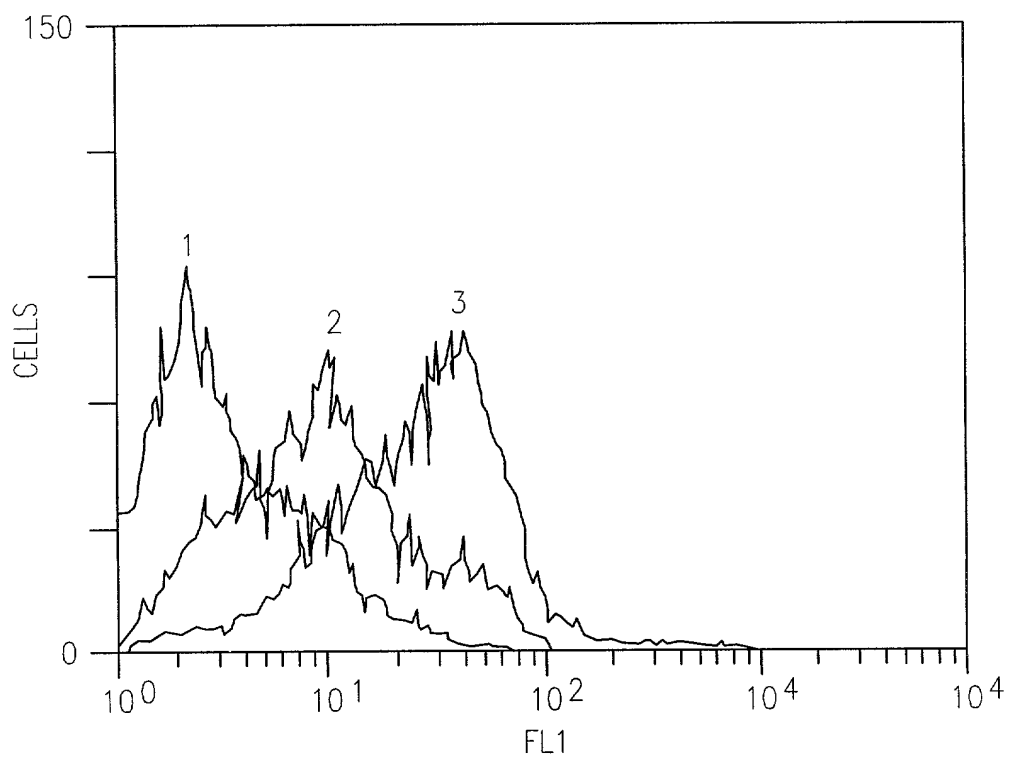


FIG. 29B

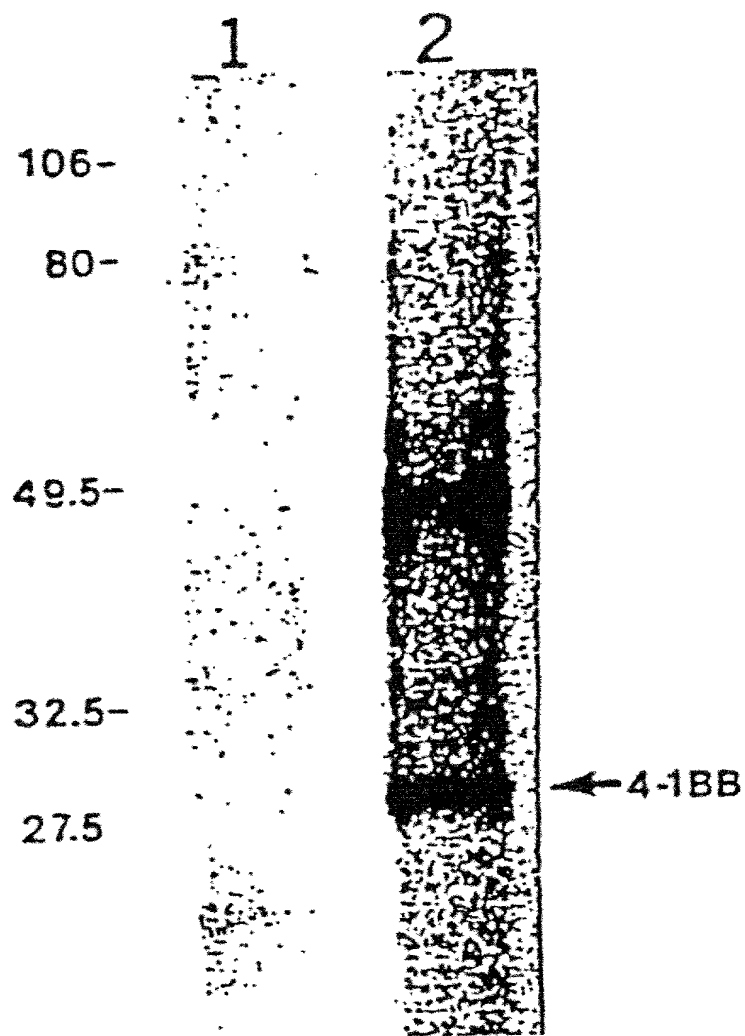


FIG. 29C

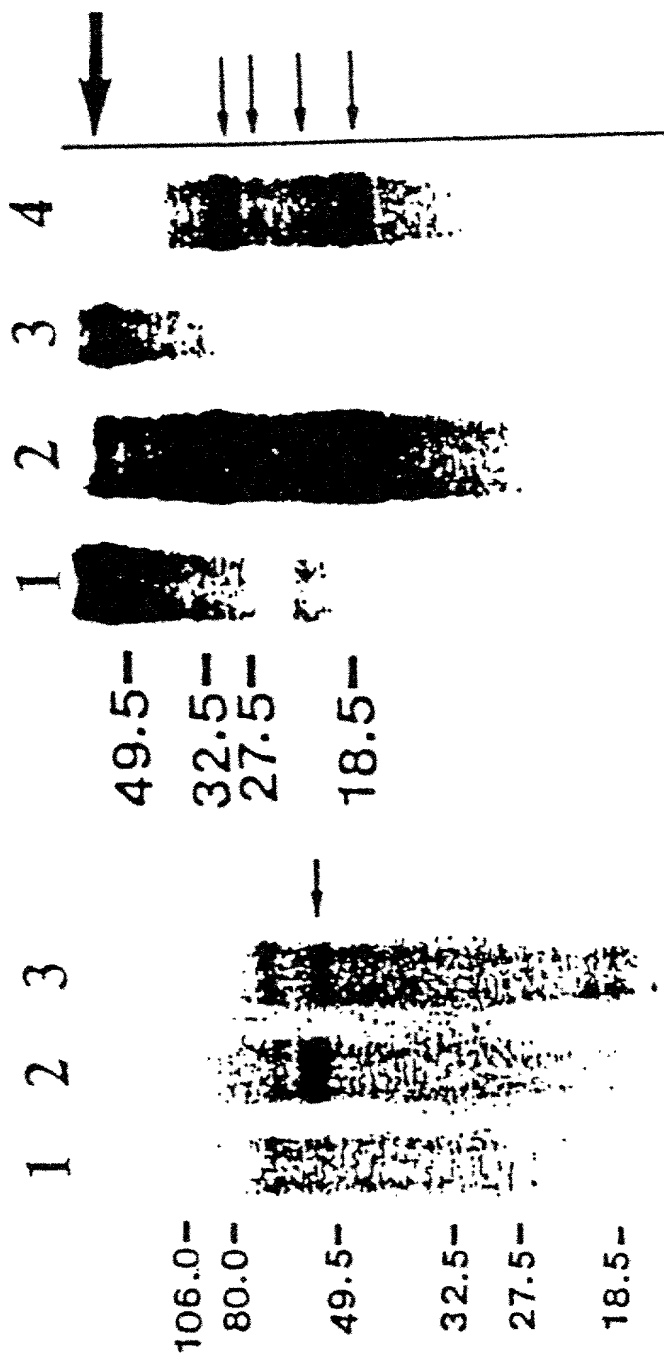


FIG. 30A

FIG. 30B

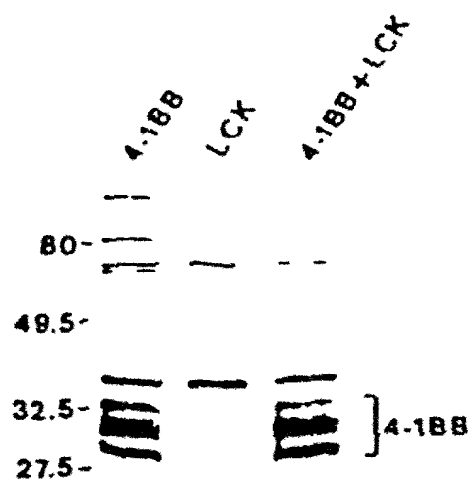


FIG. 31A

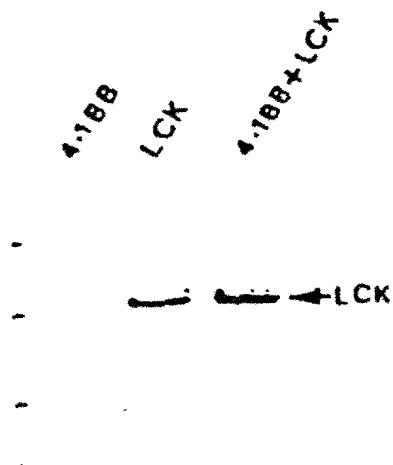


FIG. 31B

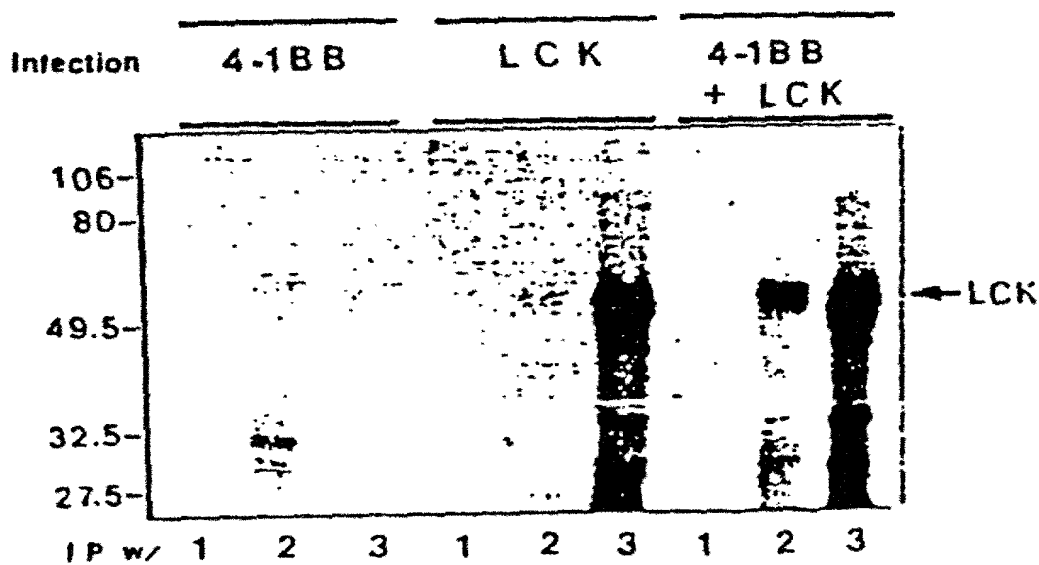


FIG. 31C

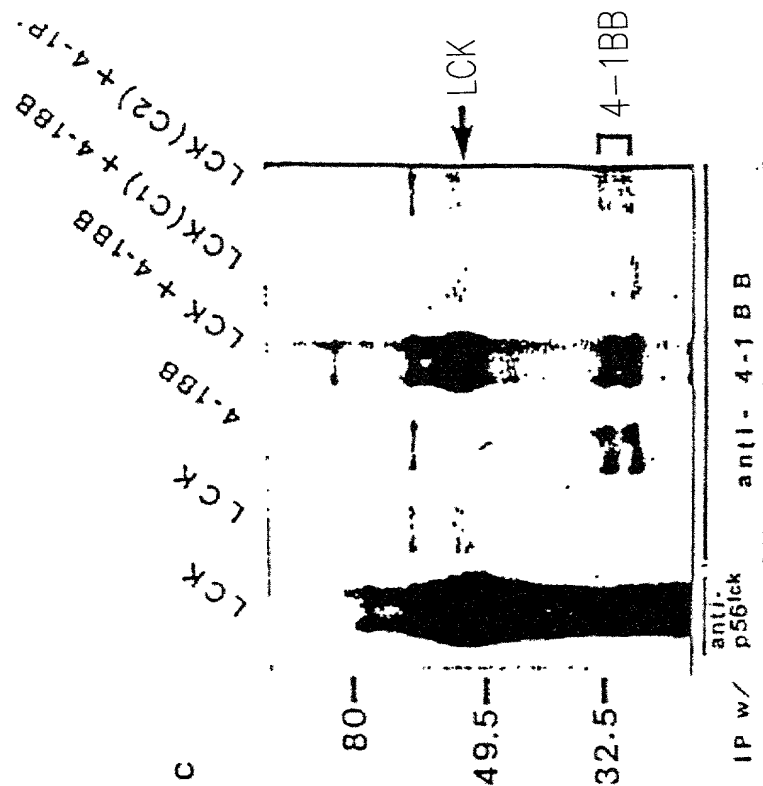


FIG. 32B

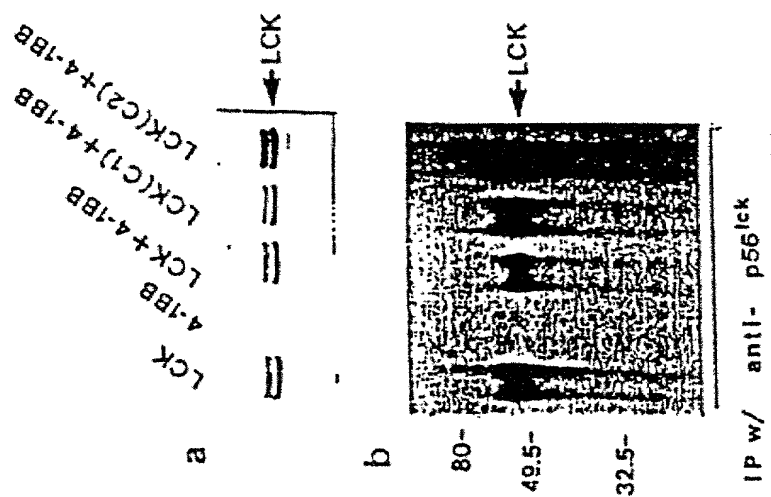


FIG. 32A



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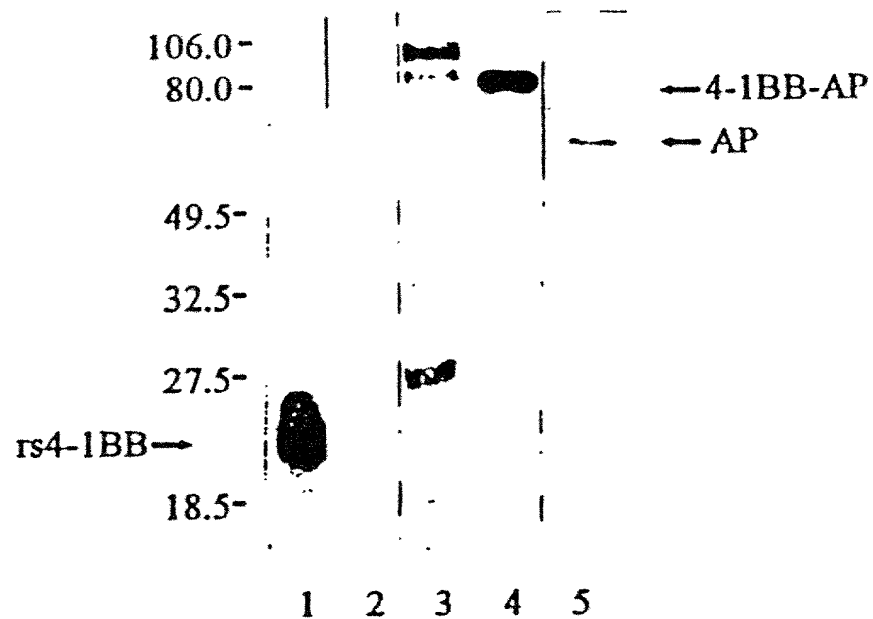


FIG. 33

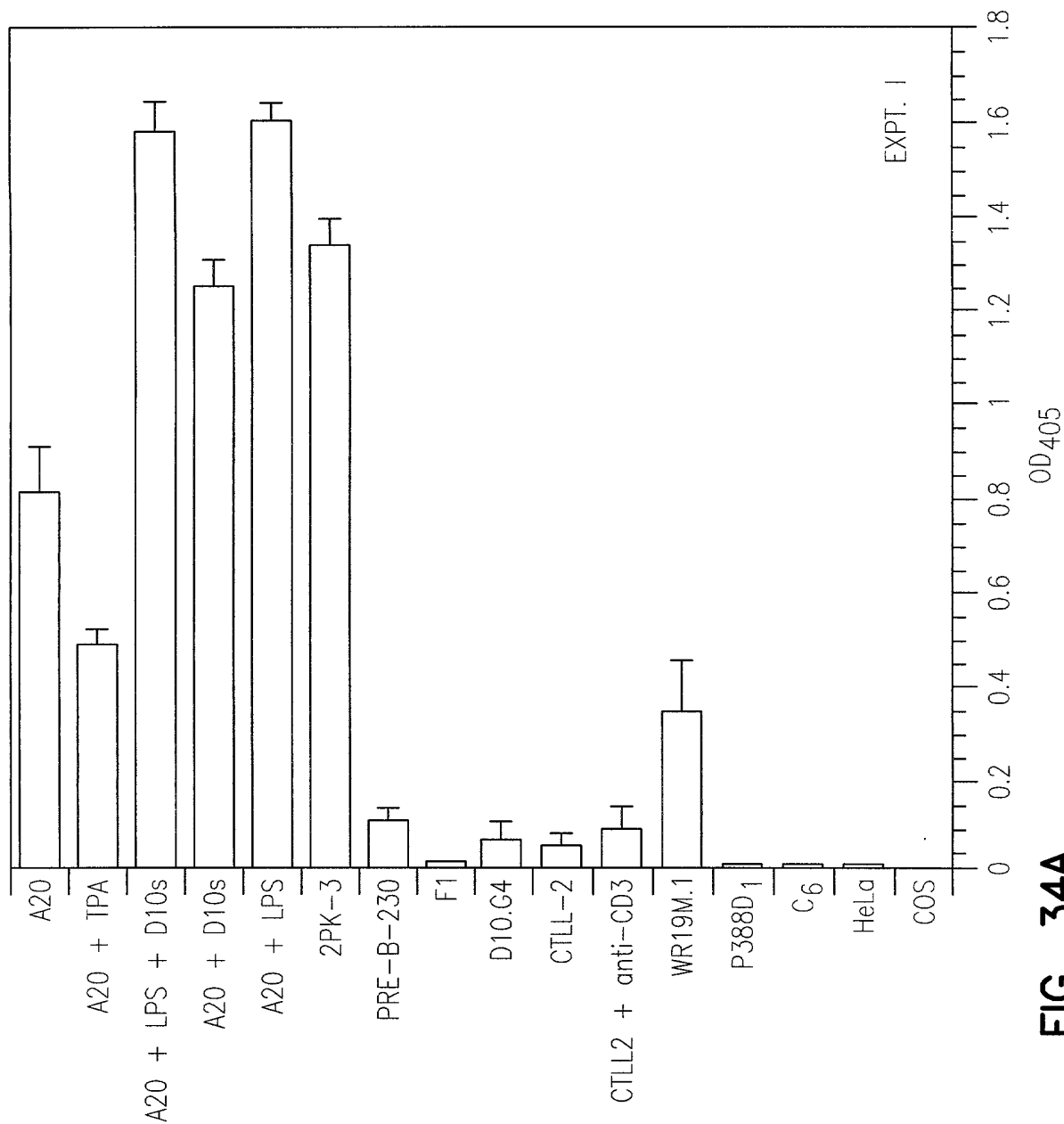


FIG. 34A

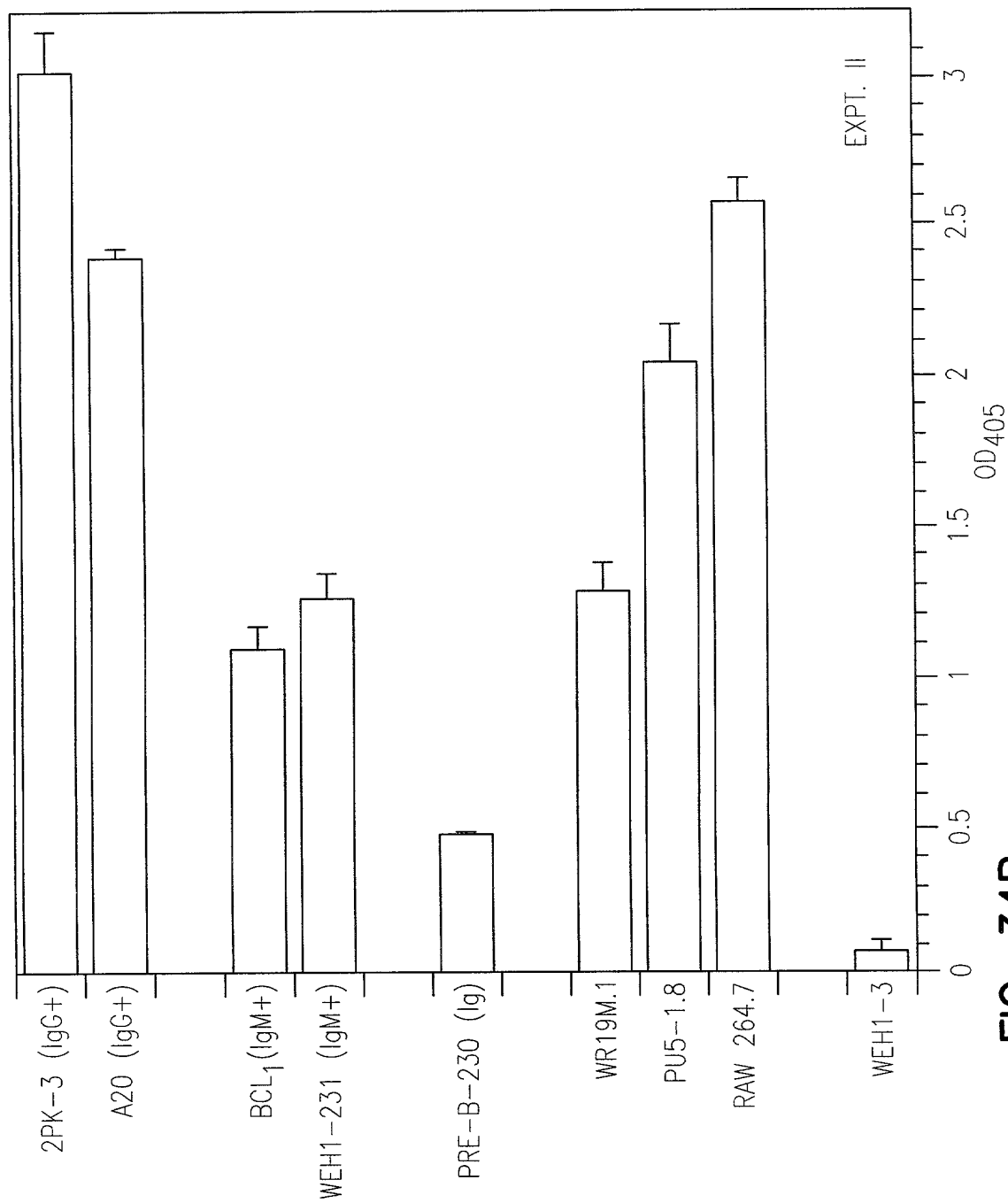


FIG. 34B

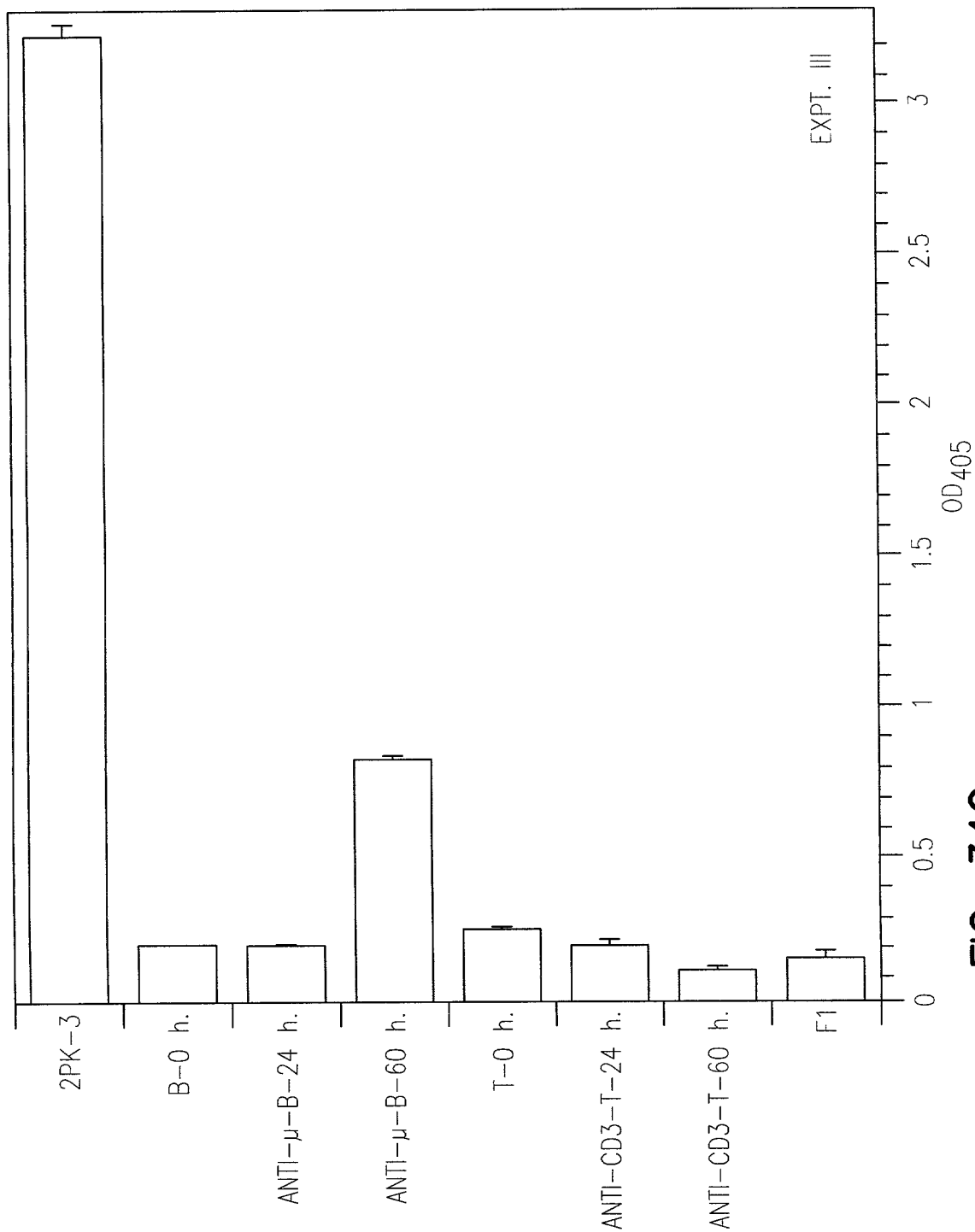


FIG. 34C

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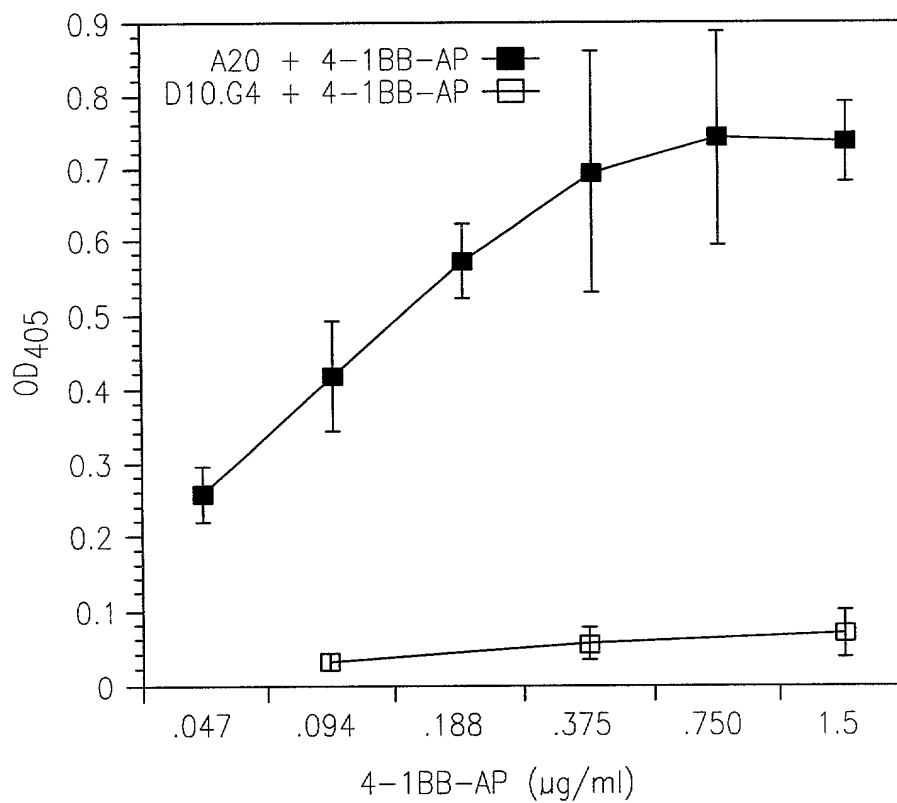


FIG. 35A

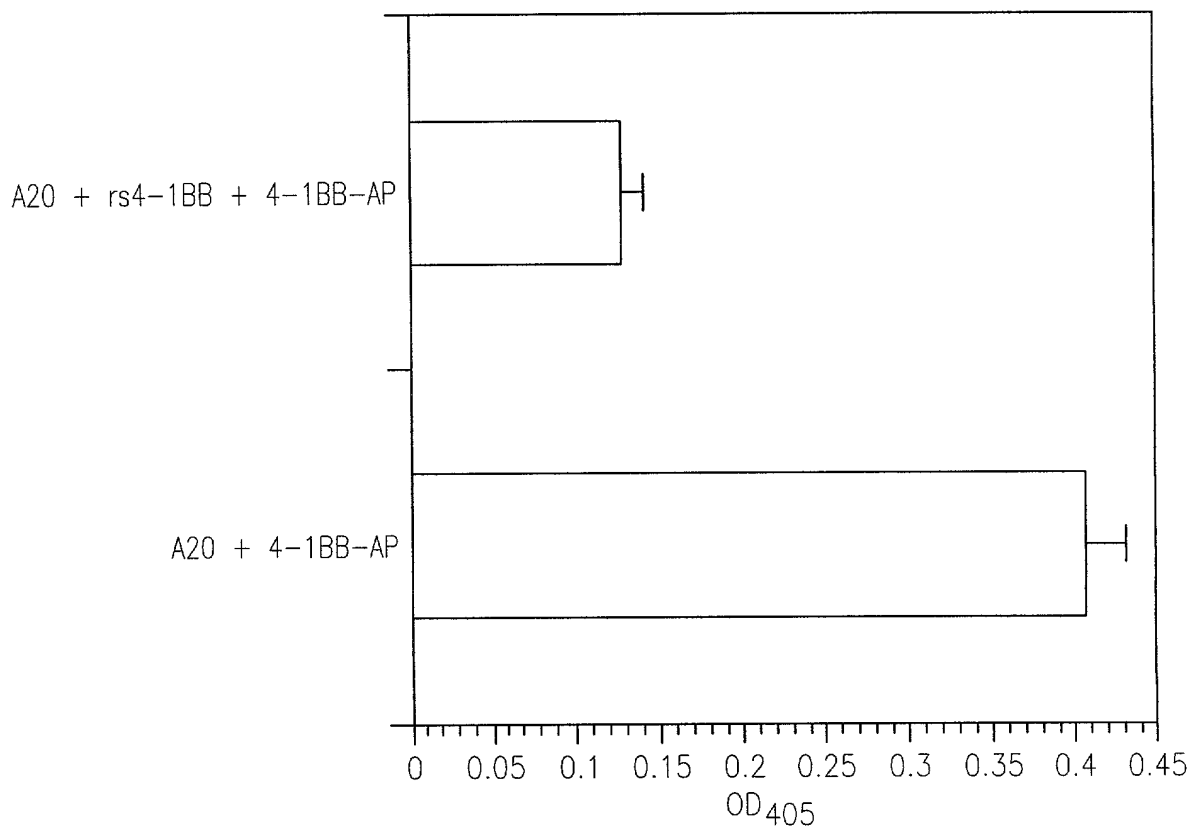


FIG. 35B

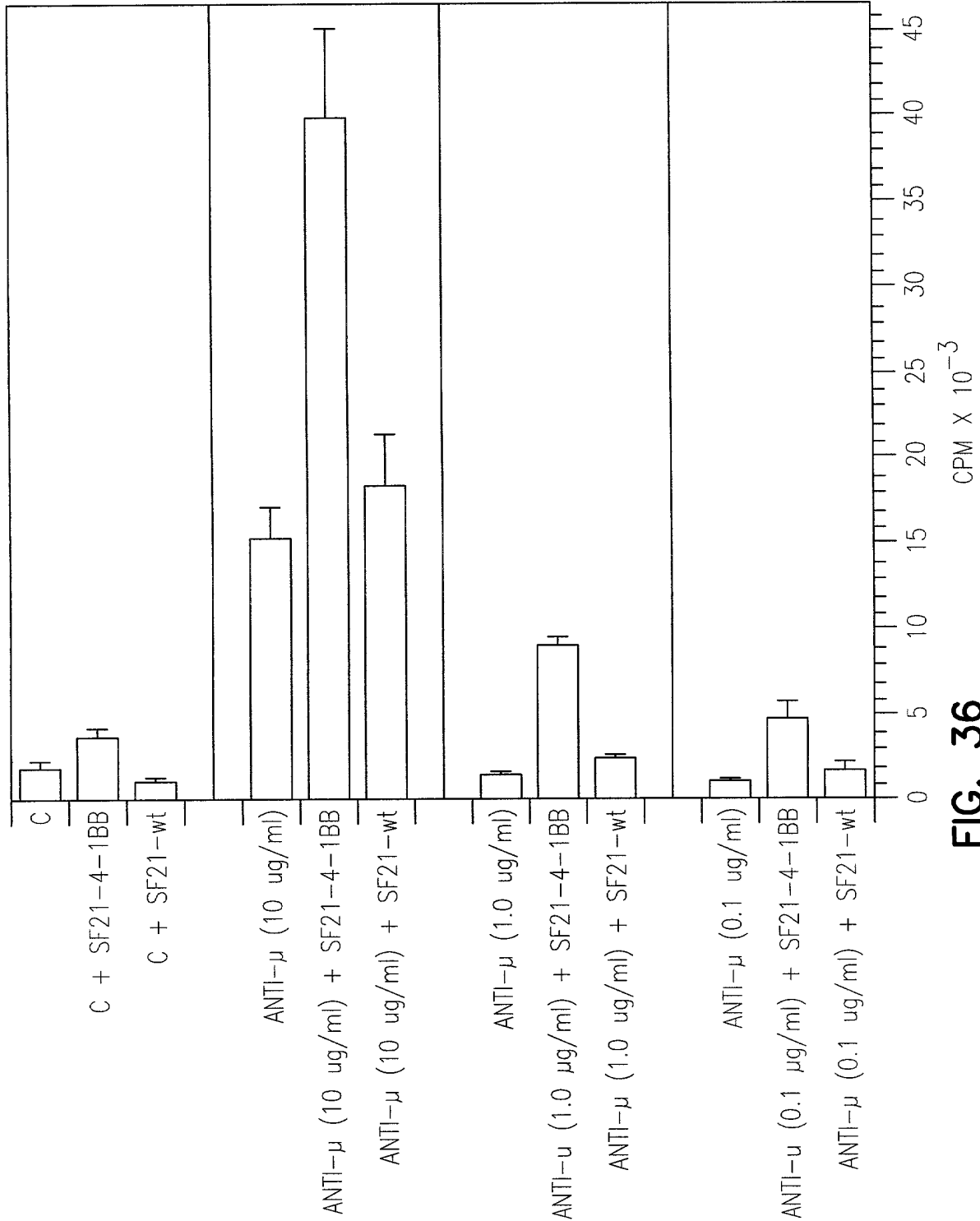


FIG. 36